

OM protein - protein search, using SW model

Run on: September 9, 2004, 13:5:20 ; Search time 32 Seconds
 (without alignments)
 327.502 Million cell updates/sec

Title: US-09-869-566-5
 Perfect score: 1059
 Sequence: 1 MSALLILAVGAAVADYKDD.....IIFSFQPVCKAAMSPEVSD 203

Scoring table: BIOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : ISSUED_PATENTS_AA:*

1: /cgn2_6/ptcdata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptcdata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptcdata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptcdata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptcdata/2/iaa/6C_COMB.pep:*

6: /cgn2_6/ptcdata/2/iaa/backtile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	895	84.5	218	4 US-09-293-625-2 Sequence 2, Appli
2	895	84.5	218	4 US-09-298-412B-4 Sequence 4, Appli
3	863.5	81.5	218	4 US-09-298-412B-2 Sequence 2, Appli
4	702	66.3	167	3 US-09-28-155-2 Sequence 7, Appli
5	695	65.6	136	3 US-09-28-155-7 Sequence 2, Appli
6	695	65.6	136	3 US-09-28-155-11 Sequence 11, Appli
7	623	58.8	115	3 US-09-28-155-5 Sequence 5, Appli
8	623	58.8	115	3 US-09-28-155-9 Sequence 9, Appli
9	623	58.8	115	3 US-09-28-155-13 Sequence 13, Appli
10	473.5	44.7	185	3 US-09-28-155-18 Sequence 18, Appli
11	229.5	21.7	169	3 US-09-290-032-2 Sequence 2, Appli
12	229.5	21.7	169	3 US-09-059-619-2 Sequence 2, Appli
13	229.5	21.7	169	4 US-09-444-018-2 Sequence 2, Appli
14	229.5	21.7	169	4 US-09-98-412B-15 Sequence 15, Appli
15	191.5	18.1	156	4 US-09-398-412B-13 Sequence 13, Appli
16	174.5	16.5	155	3 US-09-417-425-5 Sequence 5, Appli
17	174.5	16.5	155	4 US-09-348-942-5 Sequence 5, Appli
18	174.5	16.5	155	4 US-09-316-081-5 Sequence 5, Appli
19	174.5	16.5	155	4 US-09-518-458-5 Sequence 5, Appli
20	174.5	16.5	155	4 US-09-522-96A-4 Sequence 5, Appli
21	174.5	16.5	155	4 US-09-457-626-5 Sequence 5, Appli
22	174.5	16.5	155	4 US-09-516-008-5 Sequence 5, Appli
23	171	16.1	150	4 US-09-98-412B-14 Sequence 14, Appli
24	167	15.8	178	3 US-09-000-630C-21 Sequence 21, Appli
25	167	15.8	178	3 US-08-892-720C-21 Sequence 21, Appli
26	167	15.8	178	3 US-09-417-455-9 Sequence 9, Appli
27	15.8	178	4	US-09-348-942-9 Sequence 9, Appli

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; RESULT 1
; US-09-293-625-2
; Sequence 2, Application US/09293625
; Patent No. 6342371
; GENERAL INFORMATION:
; APPLICANT: Young, Peter R.
; APPLICANT: McDonnell, Peter C
; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, IL-1H4
; FILE REFERENCE: GP-70607
; CURRENT APPLICATION NUMBER: US/09/293, 625
; CURRENT FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-293-625-2

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; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 218
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
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 US-09-398-412B-4
 Query Match 84.5%; Score 895; DB 4; Length 218;
 Best Local Similarity 100.0%; Pred. No. 9. 4e-97; Mismatches 0; Indels 0; Gaps 0;
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 QY 35 PKVKNLNPKFSIHDDHKVLUVDLDSGNLJAVPDKNYTRPEIFFALASSLSSAEEKSPLI 94
 Db 50 PKVKNLNPKFSIHDDHKVLUVDLDSGNLJAVPDKNYTRPEIFFALASSLSSAEEKSPLI 109
 QY 95 LGVSKGFCLYCDKKGQSHPSLQLKQKLMQKESARPPFITYRAQGSWMLLES 154
 Db 110 LGVSKGFCLYCDKKGQSHPSLQLKQKLMQKESARPPFITYRAQGSWMLLES 169
 ;
 US-09-398-412B-2
 ; Sequence 2, Application US/09398412B
 ; Patent No. 6680380
 ; GENERAL INFORMATION:
 ; APPLICANT: Timans, Jacqueline C.
 ; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reage
 ; TITLE OF INVENTION: methods
 ; FILE REFERENCE: DX0904K
 ; CURRENT APPLICATION NUMBER: US/09/398,412B
 ; PRIORITY FILING DATE: 1999-09-17
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 218
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
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 US-09-398-412B-2
 Query Match 84.5%; Score 863.5; DB 4; Length 218;
 Best Local Similarity 84.7%; Pred. No. 4.7e-93; Mismatches 5; Indels 11; Gaps 15; Cags 2;
 Matches 172; Conservative 5; Mismatches 11; Indels 15; Gaps 2;
 ;
 QY 16 DYKDDDKLKA--AANSALCRGP-----KVNQNLPKFSIHDDHKVLUVDLGS 60
 Db 16 DWKEDEPQCCLEDPAGSPLPEPGSPSLPTKMNPFVHTSRKVKSLNPKFSIHDDHKVLUVDLGS 75
 QY 61 NLIAVDPKNYTRPEIFFALASSLSSAEEKSPLIILGVSKGFCLYCDKKGQSHPSLQL 120
 Db 76 NLIAVDPKNYTRPEIFFALASSLSSAEEKSPLIILGVSKGFCLYCDKKGQSHPSLQL 135
 QY 121 KERKLMKLAQKESARRPFFYRAQGSWMLLESAAHGPWFCITSNCNEPYGVTDKPN 180
 Db 136 KERKLMKLAQKESARRPFFYRAQGSWMLLESAAHGPWFCITSNCNEPYGVTDKPN 195
 QY 181 RKEIFSFQPVKAEMSPEVSD 203
 Db 196 RKEIFSFQPVKAEMSPEVSD 218
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 RESULT 4
 US-09-128-155-7
 ; Sequence 7, Application US/09128155
 ; Patent No. 6117654
 ; GENERAL INFORMATION:
 ; APPLICANT: Pan, Yang
 ; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
 ; FILE REFERENCE: 09404/052001
 ; CURRENT APPLICATION NUMBER: US/09/128,155
 ; PRIORITY FILING DATE: 1998-09-03
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 178
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
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 US-09-128-155-2
 Query Match 66.3%; Score 702; DB 3; Length 178;
 Best Local Similarity 93.6%; Pred. No. 3. 1e-74; Mismatches 5; Indels 0; Gaps 0;
 Matches 131; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
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 QY 64 AVPDKNYTRPEIFFALASSLSSAEEKSPLIILGVSKGFCLYCDKKGQSHPSLQLKE 123
 Db 39 SLPTMNFWHTKFFALASSLSSAEEKSPLIILGVSKGFCLYCDKKGQSHPSLQLKE 98
 QY 124 KLMKLAQKESARRPFFYRAQGSWMLLESAAHGPWFCITSNCNEPYGVTDKFNRRKH 183
 Db 99 KLMKLAQKESARRPFFYRAQGSWMLLESAAHGPWFCITSNCNEPYGVTDKFNRRKH 158
 QY 184 IERSFQPVKAEMSPEVSD 203
 Db 159 IERSFQPVKAEMSPEVSD 178

RESULT 6
US-09-128-155-11
; Sequence 11, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-128-155-11

Query Match 65.6%; Score 695; DB 3; Length 136;
Best Local Similarity 96.3%; Pred. No. 1.4e-73; Indels 0; Gaps 0;
Matches 130; Conservative 3; Mismatches 2;

Qy 69 NYIRPPIFFALASSLASSAEGSPILLGVSKGERFLYCDKDKQOSHPSLQLKEKLMKL 128
Db 2 NFRVHTRKFFALASSLASSAEGSPILLGVSKGERFLYCDKDKQOSHPSLQLKEKLMKL 61

Qy 129 AAKQESARRPPIFYRAQVGWNMLSAAHPGWFICTSNCNEPVGVTDKFENRKHIEFSF 188
Db 62 AAKQESARRPPIFYRAQVGWNMLSAAHPGWFICTSNCNEPVGVTDKFENRKHIEFSF 121

Qy 189 QPVCKAEMSPSEVSD 203
Db 122 QPVCKAEMSPSEVSD 136

RESULT 7
US-09-128-155-5
; Sequence 5, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1998-07-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-128-155-5

Query Match 65.6%; Score 695; DB 3; Length 136;
Best Local Similarity 96.3%; Pred. No. 1.4e-73; Indels 0; Gaps 0;
Matches 130; Conservative 3; Mismatches 2;

Qy 69 NYIRPPIFFALASSLASSAEGSPILLGVSKGERFLYCDKDKQOSHPSLQLKEKLMKL 128
Db 2 NFRVHTRKFFALASSLASSAEGSPILLGVSKGERFLYCDKDKQOSHPSLQLKEKLMKL 61

Qy 129 AAKQESARRPPIFYRAQVGWNMLSAAHPGWFICTSNCNEPVGVTDKFENRKHIEFSF 188
Db 62 AAKQESARRPPIFYRAQVGWNMLSAAHPGWFICTSNCNEPVGVTDKFENRKHIEFSF 121

Qy 189 QPVCKAEMSPSEVSD 203
Db 122 QPVCKAEMSPSEVSD 136

RESULT 8
US-09-128-155-9
; Sequence 9, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1998-07-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-128-155-9

Query Match 58.8%; Score 623; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 3e-65; Indels 0; Gaps 0;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; ORGANISM: Homo sapiens
; US-09-128-155-9

Query Match 58.8%; Score 623; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 3e-65; Indels 0; Gaps 0;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; ORGANISM: Homo sapiens
; US-09-128-155-9

Qy 89 EKGSPIILGVSKGERFLYCDKDKQOSHPSLQLKEKLMKLAAQESARRPPIFYRAQVG 148
Db 1 EKGSPIILGVSKGERFLYCDKDKQOSHPSLQLKEKLMKLAAQESARRPPIFYRAQVG 60

Qy 149 WNMLESAAHPGWFICTSNCNEPVGVTDKFENRKHIEFSQPVCKAEMSPSEVSD 203
Db 61 WNMLESAAHPGWFICTSNCNEPVGVTDKFENRKHIEFSQPVCKAEMSPSEVSD 115

RESULT 10
 US-09-128-155-18
 Sequence 18, Application US/09128155
 ; Paten No. 6117654
 ; GENERAL INFORMATION:
 ; APPLICANT: Pan, Yang
 ; TITLE OF INVENTION: NOVEL MOLECULES OF TAN-30-77 RELATED PROTEIN FAMILY
 ; FILE REFERENCE: 09404/052001
 ; CURRENT APPLICATION NUMBER: US/09/128 155
 ; CURRENT FILING DATE: 1998-08-03
 ; EARLIER APPLICATION NUMBER: US 60/091, 650
 ; EARLIER FILING DATE: 1998-07-02
 ; EARLIER FILING DATE: 1997-08-04
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 18
 LENGTH: 185
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 NAME/KEY: synthetically generated
 LOCATION: (1)..(185)
 OTHER INFORMATION: human sequence predicted using an alignment algorithm which
 OTHER INFORMATION: predicts presence of alternatively spliced exons for a protein of
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (1)..(185)
 OTHER INFORMATION: Xaa = Any Amino Acid
 ; US-09-128-155-18

Query Match Best Local Similarity 91.8%; Score 473.5; DB 3; Length 185; Matches 90; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

Qy 79 LASSLSSAASEKGSPILLGVSKGEFCFLXCDKQGQSHPSLQKKEKLMKLAQKESARRP 138
 Db 71 LSSLQRSAAEKGSPILLGVSKGEFCFLXCDKQGQSHPSLQKKEKLMKLAQKESARRP 129

Qy 139 PTFYRAQVGSMWNLLESAAHPGFICITSNCNPVGVTD 175
 Db 130 PTFYRAQVGSMWNLLESAAHPGFICITSNCNPVGIXN 167

RESULT 11
 US-08-790-012-2
 Sequence 2, Application US/08790032
 ; Patent No. 5833769
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, Peter
 ; TITLE OF INVENTION: Interleukin-1 Receptor Antagonist
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SmithKline Beecham Corporation
 ; STREET: 709 Swedeland Road
 ; CITY: King of Prussia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19406-0939
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/069, 619
 ; FILING DATE: Herewith
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 09/007, 464; and 08/790, 032
 ; FILING DATE: filed 14-JAN-1998; and 28-JAN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Han, William, T.
 ; REGISTRATION NUMBER: 34, 344
 ; REFERENCE/DOCKET NUMBER: ATG50051-2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-270-5090
 ; TELEX: 610-270-5090

Query Match Best Local Similarity 21.7%; Score 229.5; DB 2; Length 169; Matches 56; Conservative 29; Mismatches 62; Indels 13; Gaps 5;

Qy 19 DDDKKLAANSALCGRPKVKUNPKPSIHPDKHVLVLDGNTIAVPDKVYIRPESIFFA 78
 Db 7 DADGGGRAVYOSMCK----PTGQTLINDQQWVTLQGQNLVAVPRSDSVTPVAV 58

Qy 79 LASSLSSAASEKGSPILLGVSKGEFCFLXCDKQGQSHPSIQLKEKLMKLAQKESARR 137
 Db 59 ITCKYPKALEQGRGDPYLGIQNPEWCLYCEKVGEG---PTLQKBEKIMDLYGQPERPV-X 115

Qy 138 PTFYRAQVGSMWNLLESAAHPGFICITSNCNPVGVTDK 177
 Db 116 PTFYRAQVGSMWNLLESAAHPGFICITSNCNPVGIXN 154

RESULT 12
 US-09-069-619-2
 Sequence 2, Application US/09069619
 ; Patent No. 6054559
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, Peter and Lisa Marshall
 ; TITLE OF INVENTION: Interleukin-1 Receptor Antagonist
 ; TITLE OF INVENTION: Beta (IL-1RA)
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SmithKline Beecham Corporation
 ; STREET: 709 Swedeland Road
 ; CITY: King of Prussia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19406-0939
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/069, 619
 ; FILING DATE: Herewith
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 09/007, 464; and 08/790, 032
 ; FILING DATE: filed 14-JAN-1998; and 28-JAN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Han, William, T.
 ; REGISTRATION NUMBER: 34, 344
 ; REFERENCE/DOCKET NUMBER: ATG50051-2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-270-5090
 ; TELEX: 610-270-5090

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 169 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLogy: linear
; MOLECULE TYPE: protein
; US-09-069-619-2

Query Match 21.7%; Score 229.5; DB 3; Length 169;
Best Local Similarity 35.0%; Pred. No. 7.5e-19;
Matches 56; Conservative 29; Mismatches 62; Indels 13; Gaps 5;
QY 19 DDDDKLAAANSALCRGPKVKNLNPKKFSIHODHKVVLVDSGNLIAVPDKNYIREIFFA 78
Db 7 DADGGGRAYVQSMCK-----PITGTINDLNQQWVTLQGQNLIVAPVRSDSVPTVAV 58

Query Match 21.7%; Score 229.5; DB 4; Length 169;
Best Local Similarity 35.0%; Pred. No. 7.5e-19;
Matches 56; Conservative 29; Mismatches 62; Indels 13; Gaps 5;
QY 79 LASSLSSASAB-KSPILLGVSKGERCFLYCDKDGQSHRSIOLKKEKLMKLAOKESARR 137
Db 59 ITCKYVPEALBQGRGPDIYLGQNPWMCYCEKVGQO--PILQLKEQKIMDLYGPEPV-K 115

Query Match 21.7%; Score 229.5; DB 4; Length 169;
Best Local Similarity 35.0%; Pred. No. 7.5e-19;
Matches 56; Conservative 29; Mismatches 62; Indels 13; Gaps 5;
QY 138 PFIYRAQGVSNMLESAAHGPWFCITSNCNEPGVTDK 177
Db 116 PFLFRAKTORTSSTLESVAPPDWFIASS-KRDQPIILSE 154

RESULT 13
US-09-494-018-2
; Sequence 2, Application US/09494018
; Patent No. 6399573

GENERAL INFORMATION:
APPLICANT: Peter R. Young
TITLE OF INVENTION: INTERLEUKIN-1 RECEPTOR ANTAGONIST BBTA
FILE REFERENCE: ATG-50051-D1

CURRENT APPLICATION NUMBER: US/09/494,018
CURRENT FILING DATE: 2000-01-28
EARLIER APPLICATION NUMBER: 09/069, 619
EARLIER FILING DATE: 1998-04-29
EARLIER APPLICATION NUMBER: 09/007, 464
EARLIER FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 08/7790, 032
EARLIER FILING DATE: 1997-01-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 169
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-494-018-2

Query Match 21.7%; Score 229.5; DB 4; Length 169;
Best Local Similarity 35.0%; Pred. No. 7.5e-19;
Matches 56; Conservative 29; Mismatches 62; Indels 13; Gaps 5;
QY 19 DDDDKLAAANSALCRGPKVKNLNPKKFSIHODHKVVLVDSGNLIAVPDKNYIREIFFA 78
Db 7 DADGGGRAYVQSMCK-----PITGTINDLNQQWVTLQGQNLIVAPVRSDSVPTVAV 58

RESULT 14
US-09-398-412B-15
; Sequence 15, Application US/09398412B
; Patent No. 6680380

GENERAL INFORMATION:
APPLICANT: Jacqueline C.
TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reager
FILE REFERENCE: DX0904K

CURRENT APPLICATION NUMBER: US/09/398, 412B
CURRENT FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: US 60/100948
PRIOR FILING DATE: 1998-09-18
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 156
TYPE: PRT
ORGANISM: Mus musculus
US-09-398-412B-13

Query Match 18.1%; Score 191.5; DB 4; Length 156;
Best Local Similarity 35.1%; Pred. No. 1.9e-14;
Matches 53; Conservative 24; Mismatches 51; Indels 23; Gaps 6;
QY 79 LASSLSSASAB-KSPILLGVSKGERCFLYCDKDGQSHRSIOLKKEKLMKLAOKESARR 137
Db 59 ITCKYVPEALBQGRGPDIYLGQNPWMCYCEKVGQO--PILQLKEQKIMDLYGPEPV-K 115

Query Match 18.1%; Score 191.5; DB 4; Length 156;
Best Local Similarity 35.1%; Pred. No. 1.9e-14;
Matches 53; Conservative 24; Mismatches 51; Indels 23; Gaps 6;
QY 86 ASAKGSPIILGVSKGERCFLYCDKDGQSHRSIOLKKEKLMKLAOKESARR 144
Db 53 ASL--SPVILGVQGGSOCISCGTEKG--PILKLEPVNIMELYLGAKES--KSFTYRR 104

Query Match 14.5%; Score 175; DB 4; Length 156;
Best Local Similarity 35.1%; Pred. No. 1.9e-14;
Matches 53; Conservative 24; Mismatches 51; Indels 23; Gaps 6;
QY 145 QVGSNMLESAAHGPWFCITSNCNEPGVTDK 175
Db 105 DMGUTSSPESAAVPGWFELTSPEADQPVRLT 135

RESULT 15
US-09-398-412B-13
; Sequence 13, Application US/09398412B
; Patent No. 6680380

GENERAL INFORMATION:
APPLICANT: Jacqueline C.
TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reager
FILE REFERENCE: DX0904K

CURRENT APPLICATION NUMBER: US/09/398, 412B
CURRENT FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: US 60/100948
PRIOR FILING DATE: 1998-09-18
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 156
TYPE: PRT
ORGANISM: Mus musculus
US-09-398-412B-13

Query Match 18.1%; Score 191.5; DB 4; Length 156;
Best Local Similarity 35.1%; Pred. No. 1.9e-14;
Matches 53; Conservative 24; Mismatches 51; Indels 23; Gaps 6;
QY 28 NSALCRGPKVKNLNPKKFSIHODHKVVLVDSGNLIA--VPDKNYIREIFFALASSS 85
Db 5 SGAIC-----FRKDSALKVJYLNHQLLAGSLHAEKVIKOEEISVPNRALD 52

Query Match 14.5%; Score 175; DB 4; Length 156;
Best Local Similarity 35.1%; Pred. No. 1.9e-14;
Matches 53; Conservative 24; Mismatches 51; Indels 23; Gaps 6;
QY 86 ASAKGSPIILGVSKGERCFLYCDKDGQSHRSIOLKKEKLMKLAOKESARR 144
Db 53 ASL--SPVILGVQGGSOCISCGTEKG--PILKLEPVNIMELYLGAKES--KSFTYRR 104

RESULT 16
US-09-398-412B-15
; Sequence 16, Application US/09398412B
; Patent No. 6680380

GENERAL INFORMATION:

Search completed: September 9, 2004, 13:29:59
Job time : 33 secs

GenCore version 5.1.6
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On protein - protein search, using sw model

Run on: September 9, 2004, 13:23:09 ; Search time 48 Seconds

(without alignments)
 1356.250 Million cell updates/sec

Title: US-09-869-566-5

Perfect score: 1059

Sequence: 1 MSALLIALVGRAVADYKDD.....IEFSFQFQVKAEMSPESEVD 203

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1335176 Beqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaal/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaal/PCT_NEW_PUB_pep:*

3: /cgn2_6/ptodata/2/pubpaal/US05_PUBCOMB.pep:*

4: /cgn2_6/ptodata/2/pubpaal/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaal/US07_NEW_PUB_pep:*

6: /cgn2_6/ptodata/2/pubpaal/PCTUS_PUBCOMB.pep:*

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11: /cgn2_6/ptodata/2/pubpaal/US10_PUBCOMB.pep:*

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14: /cgn2_6/ptodata/2/pubpaal/US10_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaal/US10_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaal/US10_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaal/US10_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaal/US10_PUBCOMB.pep:*

RESULT 1

US-09-876-790-3

Sequence 3, Application US/09876790

Publication No. US2003010091532A1

GENERAL INFORMATION:

APPLICANT: SIMS, John E.

APPLICANT: SMITH, Dirk E.

APPLICANT: BORN, Teresa L.

TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XREC2 DNAs AND POLYPEPTI

FILE REFERENCE: 2003-US

CURRENT APPLICATION NUMBER: US/09/876,790

CURRENT FILING DATE: 2002-09-04

PRIOR APPLICATION NUMBER: 60/112,153

PRIOR FILING DATE: 1998-12-14

PRIOR APPLICATION NUMBER: 60/146,675

PRIOR FILING DATE: 1999-11-10

PRIOR APPLICATION NUMBER: PCT/US99/29549

PRIOR FILING DATE: 1999-12-14

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin version 3.1.1
 SEQ ID NO 3
 LENGTH: 192

TYPE: PRT

ORGANISM: Homo sapiens

US-09-876-790-3

Query Match 85.6%; Score 906; DB 10; Length 192;

Best Local Similarity 100.0%; Score 906; DB 10; Length 192;

Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

33 RGPKYKNLMPKKSIHDOPHKVILDSLNLIAPDKNTIRPEFFALSSLSSAEGGS 92

||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

22 RGPKVKNLMPKKSIHDOPHKVILDSLNLIAPDKNTIRPEFFALSSLSSAEGGS 81

93 PIUGVSKBFCFLCDKQGSHPSLQKKEKUMLAQKESARRPFTYRAQGSMNL 152

82 PIUGVSKBFCFLCDKQGSHPSLQKKEKUMLAQKESARRPFTYRAQGSMNL 141

16	885	83.6	193	12	US-10-063-515-142	Sequence 142, App
17	885	83.6	193	12	US-10-063-549-142	Sequence 142, App
18	885	83.6	193	12	US-10-063-569-142	Sequence 142, App
19	885	83.6	193	12	US-10-063-551-142	Sequence 142, App
20	885	83.6	193	12	US-10-063-555-142	Sequence 142, App
21	885	83.6	193	12	US-10-063-563-142	Sequence 142, App
22	885	83.6	193	12	US-10-063-594-142	Sequence 142, App
23	885	83.6	193	12	US-10-063-555-142	Sequence 142, App
24	885	83.6	193	12	US-10-063-554-142	Sequence 142, App
25	885	83.6	193	13	US-10-006-867-142	Sequence 142, App
26	885	83.6	193	13	US-10-063-542-142	Sequence 142, App
27	885	83.6	193	14	US-10-063-616-142	Sequence 142, App
28	885	83.6	193	14	US-10-063-502-142	Sequence 142, App
29	885	83.6	193	14	US-10-063-518-142	Sequence 142, App
30	885	83.6	193	14	US-10-063-580-142	Sequence 142, App
31	885	83.6	193	14	US-10-022-693-142	Sequence 142, App
32	885	83.6	193	14	US-10-063-585-142	Sequence 142, App
33	885	83.6	193	14	US-10-063-588-142	Sequence 142, App
34	885	83.6	193	14	US-10-063-599-142	Sequence 142, App
35	885	83.6	193	14	US-10-063-595-142	Sequence 142, App
36	885	83.6	193	14	US-10-063-526-142	Sequence 142, App
37	885	83.6	193	14	US-10-063-557-142	Sequence 142, App
38	885	83.6	193	14	US-10-063-585-142	Sequence 142, App
39	885	83.6	193	14	US-10-063-588-142	Sequence 142, App
40	885	83.6	193	14	US-10-063-735-142	Sequence 142, App
41	885	83.6	193	14	US-10-063-526-142	Sequence 142, App
42	885	83.6	193	14	US-10-063-586-142	Sequence 142, App
43	885	83.6	193	14	US-10-063-546-142	Sequence 142, App
44	885	83.6	193	14	US-10-063-564-142	Sequence 142, App
45	885	83.6	193	14	US-10-063-662-142	Sequence 142, App

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Length DB ID Description

1 905 85.6 192 10 US-09-876-790-3 Sequence 3, Appli

2 905 85.6 192 14 US-10-133-833-13 Sequence 13, Appli

3 902 85.2 197 10 US-09-876-790-9 Sequence 9, Appli

4 895 84.5 198 9 US-09-788-963-6 Sequence 6, Appli

5 895 84.5 218 9 US-09-788-963-2 Sequence 2, Appli

6 895 84.5 218 10 US-09-876-790-8 Sequence 8, Appli

7 895 84.5 218 12 US-10-691-95-4 Sequence 4, Appli

8 895 84.5 218 14 US-10-133-833-12 Sequence 12, Appli

9 895 84.5 218 14 US-10-302-554-2 Sequence 2, Appli

10 895 84.5 218 16 US-10-694-978-4 Sequence 4, Appli

11 895 84.5 218 16 US-10-679-201-6 Sequence 6, Appli

12 891 84.1 218 14 US-10-302-554-14 Sequence 14, Appli

13 885 83.6 193 12 US-10-063-745-142 Sequence 142, Appli

14 885 83.6 193 12 US-10-063-512-142 Sequence 142, Appli

15 885 83.6 193 12 US-10-063-513-142 Sequence 142, Appli

Sequence 2, Application US/09788963
 Patent No. US2002052473A1
 GENERAL INFORMATION:
 APPLICANT: YOUNG, PETER R.
 APPLICANT: McDONNELL, PETER C.
 APPLICANT: KUMAR, SANJAY
 TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, MAT IL-1H4
 FILE REFERENCE: GP-70607-1C1
 CURRENT APPLICATION NUMBER: US/09/788,963
 CURRENT FILING DATE: 2001-02-20
 PRIOR APPLICATION NUMBER: 09/293,625
 PRIOR FILING DATE: 1999-04-15
 PRIOR APPLICATION NUMBER: 09/452,140
 PRIOR FILING DATE: 1999-12-01
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 2
 LENGTH: 218
 TYPE: PRT
 ORGANISM: HOMO SAPIENS
 US-09-788-963-2

Query Match 84.5%; Score 895; DB 9; Length 218;
 Best Local Similarity 100.0%; Pred. No. 9,1e-90; Indels 0; Gaps 0;
 Matches 169; Conservative

Qy 35 PKVKNLNPKEFSIHODPKVLUVDGSLNIVPDKNYRPEIFFLASSSSAEGKSPI 94
 Db 50 PKVKNLNPKEFSIHODPKVLUVDGSLNIVPDKNYRPEIFFLASSSSAEGKSPI 109

Qy 95 LLGVSKEFCILYCDKDGSHPSLQLKKEKLMKLAQESARRPFFRAQVGSWNMLES 154
 Db 110 LLGVSKEFCILYCDKDGSHPSLQLKKEKLMKLAQESARRPFFRAQVGSWNMLES 169

Qy 155 AAHPGWFCITSCNCNEPVGVTDKFRKHEFSQPVCKAEMSPSEVSD 203
 Db 170 AAHPGWFCITSCNCNEPVGVTDKFRKHEFSQPVCKAEMSPSEVSD 218

RESULT 7
 US-10-695-195-4
 Sequence 4, Application US/10695195
 Publication No. US20040066099A1
 GENERAL INFORMATION:
 APPLICANT: Timans, Jacqueline C.
 TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DNAX Research Institute
 STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.3.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/695,195
 FILING DATE: 27-Oct-2003
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/398,412
 FILING DATE: 17-Sep-1999
 ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0904K

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 852-9196
 TELEFAX: (650) 496-1200

INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 218 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-10-695-195-4

Query Match 84.5%; Score 895; DB 12; Length 218;
 Best Local Similarity 100.0%; Pred. No. 9,1e-90; Indels 0; Gaps 0;
 Matches 169; Conservative

Qy 35 PKVKNLNPKEFSIHODPKVLUVDGSLNIVPDKNYRPEIFFLASSSSAEGKSPI 94
 Db 50 PKVKNLNPKEFSIHODPKVLUVDGSLNIVPDKNYRPEIFFLASSSSAEGKSPI 109

Qy 95 LLGVSKEFCILYCDKDGSHPSLQLKKEKLMKLAQESARRPFFRAQVGSWNMLES 154
 Db 110 LLGVSKEFCILYCDKDGSHPSLQLKKEKLMKLAQESARRPFFRAQVGSWNMLES 169

Qy 155 AAHPGWFCITSCNCNEPVGVTDKFRKHEFSQPVCKAEMSPSEVSD 203
 Db 170 AAHPGWFCITSCNCNEPVGVTDKFRKHEFSQPVCKAEMSPSEVSD 218

RESULT 8
 US-10-139-833-12
 Sequence 12, Application US/10139833
 Publication No. US2003004106A1

Query Match 84.5%; Score 895; DB 10; Length 218;
 Best Local Similarity 100.0%; Pred. No. 9,1e-90; Indels 0; Gaps 0;
 Matches 169; Conservative

Qy 35 PKVKNLNPKEFSIHODPKVLUVDGSLNIVPDKNYRPEIFFLASSSSAEGKSPI 94
 Db 50 PKVKNLNPKEFSIHODPKVLUVDGSLNIVPDKNYRPEIFFLASSSSAEGKSPI 109

GENERAL INFORMATION:

APPLICANT: Saxis, Christiana M.
APPLICANT: Giles, Jennifer
APPLICANT: Mu, Sharon X.
APPLICANT: Xia, Min
APPLICANT: Bass, Michael B.
APPLICANT: Craveiro, Roger
TITLE OF INVENTION: Interleukin-1 Receptor Antagonist-Related Molecules and
FILE REFERENCE: 00-1213-E
CURRENT APPLICATION NUMBER: US/10/139, 833
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 60/170, 191
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: 60/188, 053
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: 60/195, 910
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: 09/724, 583
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 37
SEQ ID NO 12
LENGTH: 218
TYPE: PRT
ORGANISM: Homo sapiens
US-10-139-833-12

Query Match 84.5%; Score 895; DB 14; Length 218;
Best Local Similarity 100.0%; Pred. No. 9.1e-90; Mismatches 0; Indels 0; Gaps 0;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 PKVKNLNPKKFSIHDDQHKVVLVDLSGNLIAVDPKNVIRPEIFFALASSLSASAEGKSPI 94
Db 50 PKVKNLNPKKFSIHDDQHKVVLVDLSGNLIAVDPKNVIRPEIFFALASSLSASAEGKSPI 109

Qy 95 LLGVSKGERFLCYCDKQGKQSHPSLQLKEKUMKLAQKESARRPFYRAQGVSNMLES 154
Db 110 LLGVSKGERFLCYCDKQGKQSHPSLQLKEKUMKLAQKESARRPFYRAQGVSNMLES 169

Qy 155 AAHPGWFICTSNCNCNBERPGVTDKFENRKHIEFSFQVCKAEMSPSEVSD 203
Db 170 AAHPGWFICTSNCNCNBERPGVTDKFENRKHIEFSFQVCKAEMSPSEVSD 218

RESULT 10
US-10-694-978-4
; Sequence 4, Application US/10/694-978
; Publication No. US20040087766A1

GENERAL INFORMATION:

APPLICANT: Timans, Jacqueline C.
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/694, 978
FILING DATE: 27-Oct-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/398, 412
FILING DATE: 17-Sep-1999
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34, 090
REFERENCE/DOCKET NUMBER: DX0904K

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 852-2196
TELEFAX: (650) 496-1200

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-694-978-4

Query Match 84.5%; Score 895; DB 16; Length 218;
Best Local Similarity 100.0%; Pred. No. 9.1e-90; Mismatches 0; Indels 0; Gaps 0;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 PKVKNLNPKKFSIHDDQHKVVLVDLSGNLIAVDPKNVIRPEIFFALASSLSASAEGKSPI 94
Db 50 PKVKNLNPKKFSIHDDQHKVVLVDLSGNLIAVDPKNVIRPEIFFALASSLSASAEGKSPI 109

Qy 95 LLGVSKGERFLCYCDKQGKQSHPSLQLKEKUMKLAQKESARRPFYRAQGVSNMLES 154
Db 110 LLGVSKGERFLCYCDKQGKQSHPSLQLKEKUMKLAQKESARRPFYRAQGVSNMLES 169

Qy 155 AAHPGWFICTSNCNCNBERPGVTDKFENRKHIEFSFQVCKAEMSPSEVSD 203
Db 170 AAHPGWFICTSNCNCNBERPGVTDKFENRKHIEFSFQVCKAEMSPSEVSD 218

Query Match 84.5%; Score 895; DB 14; Length 218;
Best Local Similarity 100.0%; Pred. No. 9.1e-90; Mismatches 0; Indels 0; Gaps 0;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
 US-10-679-201-6
 ; Sequence 6, Application US/10679201
 ; Publication No. US2004012023A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DINARELLO, CHARLES A.
 ; APPLICANT: KIM, SOO-HYUN
 ; APPLICANT: BUFFLER, PHILIP
 ; TITLE OF INVENTION: METHOD OF TREATMENT USING A CYTOKINE ABLE TO BIND
 ; FILE REFERENCE: 057878-000011
 ; CURRENT APPLICATION NUMBER: US/10/679, 201
 ; CURRENT FILING DATE: 2003-10-03
 ; PRIOR APPLICATION NUMBER: 6/0416, 827
 ; PRIOR FILING DATE: 2002-10-08
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 6
 ; LENGTH: 218
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-679-201-6

Query Match 84.5%; Score 895; DB 16; Length 218;
 Best local Similarity 100.0%; Pred. No. 9.1e-90; Mismatches 0; Indels 0; Gaps 0;
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 PKVKQNLNPKPSIHDQDKVVLVLDSGNLAVPDKNYIRPPIFFALASSSSASAEGSPI 94
 50 PKVKQNLNPKPSIHDQDKVVLVLDSGNLAVPDKNYIRPPIFFALASSSSASAEGSPI 109

QY 95 LGVSKGEFLYCDKDGKQHPSLQLKKLMAQKESARRPPIFYRAQGVSNMLES 154
 110 LGVSKGEFLYCDKDGKQHPSLQLKKLMAQKESARRPPIFYRAQGVSNMLES 169

QY 155 AHPGWFICTSCNCNEPVGVTDKFENRKHIEFSQFOPVCKAEMSSEVSD 203
 170 AHPGWFICTSCNCNEPVGVTDKFENRKHIEFSQFOPVCKAEMSSEVSD 218

RESULT 12
 US-10-302-554-14
 ; Sequence 14, Application US/10302554
 ; Publication No. US20030148467A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wett, Robert R.
 ; APPLICANT: Gao, Zeren
 ; APPLICANT: Sheppard, Paul O.
 ; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOG ZILIA4
 ; CURRENT APPLICATION NUMBER: US/10/302, 554
 ; CURRENT FILING DATE: 2002-11-22
 ; PRIOR APPLICATION NUMBER: US/09/428, 118
 ; PRIOR FILING DATE: 1999-10-27
 ; PRIOR APPLICATION NUMBER: US 60/105, 824
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 14
 ; LENGTH: 218
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: variant protein
 US-10-302-554-14

Query Match 84.1%; Score 891; DB 14; Length 218;
 Best Local Similarity 99.4%; Pred. No. 2.5e-89; Mismatches 0; Indels 0; Gaps 0;

QY 36 KVVKQNLNPKPSIHDQDKVVLVLDSGNLAVPDKNYIRPPIFFALASSSSASAEGSPI 95
 26 RVVKQNLNPKPSIHDQDKVVLVLDSGNLAVPDKNYIRPPIFFALASSSSASAEGSPI 85

QY 96 LGVSKGEFLYCDKDGKQHPSLQLKKLMAQKESARRPPIFYRAQGVSNMLES 155
 86 LGVSKGEFLYCDKDGKQHPSLQLKKLMAQKESARRPPIFYRAQGVSNMLES 145

QY 156 AHPGWFICTSCNCNEPVGVTDKFENRKHIEFSQFOPVCKAEMSSEVSD 203
 146 AHPGWFICTSCNCNEPVGVTDKFENRKHIEFSQFOPVCKAEMSSEVSD 193

RESULT 14
 US-10-063-512-142
 ; Sequence 142, Application US/0063512
 ; Publication No. US200300183A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.

QY 95 LGVSKGEFLYCDKDGKQHPSLQLKKLMAQKESARRPPIFYRAQGVSNMLES 154
 110 LGVSKGEFLYCDKDGKQHPSLQLKKLMAQKESARRPPIFYRAQGVSNMLES 169

QY 155 AHPGWFICTSCNCNEPVGVTDKFENRKHIEFSQFOPVCKAEMSSEVSD 203
 170 AHPGWFICTSCNCNEPVGVTDKFENRKHIEFSQFOPVCKAEMSSEVSD 218

RESULT 13
 US-10-063-745-142
 ; Sequence 142, Application US/10063745
 ; Publication No. US20040058411A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.

QY 95 LGVSKGEFLYCDKDGKQHPSLQLKKLMAQKESARRPPIFYRAQGVSNMLES 154
 110 LGVSKGEFLYCDKDGKQHPSLQLKKLMAQKESARRPPIFYRAQGVSNMLES 169

QY 155 AHPGWFICTSCNCNEPVGVTDKFENRKHIEFSQFOPVCKAEMSSEVSD 203
 170 AHPGWFICTSCNCNEPVGVTDKFENRKHIEFSQFOPVCKAEMSSEVSD 218

Query Match 83.6%; Score 865; DB 12; Length 193;
 Best local Similarity 99.4%; Pred. No. 9.7e-89; Mismatches 0; Indels 0; Gaps 0;
 Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 36 KVVKQNLNPKPSIHDQDKVVLVLDSGNLAVPDKNYIRPPIFFALASSSSASAEGSPI 95
 26 RVVKQNLNPKPSIHDQDKVVLVLDSGNLAVPDKNYIRPPIFFALASSSSASAEGSPI 85

QY 96 LGVSKGEFLYCDKDGKQHPSLQLKKLMAQKESARRPPIFYRAQGVSNMLES 155
 86 LGVSKGEFLYCDKDGKQHPSLQLKKLMAQKESARRPPIFYRAQGVSNMLES 145

QY 156 AHPGWFICTSCNCNEPVGVTDKFENRKHIEFSQFOPVCKAEMSSEVSD 203
 146 AHPGWFICTSCNCNEPVGVTDKFENRKHIEFSQFOPVCKAEMSSEVSD 193

RESULT 14
 US-10-063-512-142
 ; Sequence 142, Application US/0063512
 ; Publication No. US200300183A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.

QY 95 LGVSKGEFLYCDKDGKQHPSLQLKKLMAQKESARRPPIFYRAQGVSNMLES 154
 110 LGVSKGEFLYCDKDGKQHPSLQLKKLMAQKESARRPPIFYRAQGVSNMLES 169

QY 155 AHPGWFICTSCNCNEPVGVTDKFENRKHIEFSQFOPVCKAEMSSEVSD 203
 170 AHPGWFICTSCNCNEPVGVTDKFENRKHIEFSQFOPVCKAEMSSEVSD 218

Query Match 84.1%; Score 891; DB 14; Length 218;
 Best Local Similarity 99.4%; Pred. No. 2.5e-89; Mismatches 0; Indels 0; Gaps 0;

QY 35 PKVKQNLNPKPSIHDQDKVVLVLDSGNLAVPDKNYIRPPIFFALASSSSASAEGSPI 94

; CURRENT APPLICATION NUMBER: US/10/063,512
 ; CURRENT FILING DATE: 2002-05-01
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 142
 ; LENGTH: 193
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-063-512-142

RESULT 15
 US-10-063-513-142
 ; Sequence 142, Application US/10063513
 ; Publication No. US200301018172A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gearritten, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Gozdowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Watanabe, Colin K.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEARIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P2230R.C1
 ; CURRENT APPLICATION NUMBER: US/10/063,513
 ; CURRENT FILING DATE: 2002-05-01
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 142
 ; LENGTH: 193
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-063-513-142

Query Match 83.6%; Score 885; DB 12; Length 193;
 Best Local Similarity 99.4%; Pred. No. 9.7e-89; 1; Mismatches 0; Indels 0; Gaps 0;
 Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 36 KVKNLNPKKFSTHDQDHKLVLDSGNLIAVPPKNYIRPEIFFALASSSSAASKGSPIL 95
 Db 26 RVKNLNPKKFSTHDQDHKLVLDSGNLIAVPPKNYIRPEIFFALASSSSAASKGSPIL 85
 Qy 96 LGVSKGERFLYCDKDGSHPSIQLKKERLMLKLAQKESARRPFFRAQVSNWMLESA 155
 Db 86 LGVSKGERFLYCDKDGSHPSIQLKKERLMLKLAQKESARRPFFRAQVSNWMLESA 145

Qy 156 AHGWFICITPSNCNEPVGVTDKFENRKHIEFSQPVCKAEMPSSEVSD 203
 Db 146 AHGWFICITPSNCNEPVGVTDKFENRKHIEFSQPVCKAEMPSSEVSD 193

Search completed: September 9, 2004, 13:29:22
 Job time : 50 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model
Run on: September 9, 2004, 13:11:59 ; Search time 123 Seconds
(without alignments)
466.318 Million cell updates/sec

Title: US-09-869-566-5

Perfect score: 1059

Sequence: 1 MSALILALVALVGAADVYKDD.....IEFSFQPVCKAEMSPEVSD 203

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 28254755 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: geneseq_1980s:*
- 2: geneseq_1990s:*
- 3: geneseq_2000s:*
- 4: geneseq_2001s:*
- 5: geneseq_2002s:*
- 6: geneseq_2003s:*
- 7: geneseq_2004s:*
- 8: geneseq_2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description	Key	Location/Qualifiers	ALIGNMENTS
1	1059	100.0	203	3 AAY6933	RESULT 1		
2	906	85.6	192	3 AAY95297	AYY96933	ID AAY96933 standard; protein; 203 AA.	
3	902	85.2	197	3 AAY95300	XX	XX	
4	895	84.5	198	3 AAB5138	AC	AAV96933;	
5	895	84.5	207	3 AAY95938	XX	XX	
6	895	84.5	218	3 AAY0927	DT	31-OCT-2000 (first entry)	
7	895	84.5	218	3 AAY91885	DE	Human IL-1R1a fused to heterologous signal sequence.	
8	895	84.5	218	3 AAY95299	XX	XX	
9	895	84.5	218	3 AAY95940	KW	hIL-1R1a; human interleukin-1 receptor antagonist-1; IL-1Lip; osteopathic; interleukin-1-like polypeptide; anti-inflammatory; anti-asthmatic; anti-articular; antimicrobial; respiratory; anti-ischemic; vaccine; dermatological; immunomodulatory; gastrointestinal; gene therapy.	
10	895	84.5	218	3 AAB28266	XX	XX	
11	895	84.5	218	3 AAB4186	XX	XX	
12	895	84.5	218	4 AAG6116	WO20039297-A2.		
13	895	84.5	218	4 AAB85136	XX	06-JUL-2000.	
14	892	84.2	218	3 AAY71084	XX	XX	
15	891	84.1	218	3 AAY0933	PF	22-DEC-1999; 99W0-US030720.	
16	885	83.6	193	3 AAY9594	XX	XX	
17	885	83.6	193	4 AAB87596	PR	23-DEC-1998; 98W0-0113430P.	
18	885	83.6	193	4 ABG95921	PR	13-APR-1999; 99W0-0129122P.	
19	885	83.6	193	6 ABU9946	PR	WPI: 2000-452395139.	
20	885	83.6	193	6 AB034005	DR	N-PSDB; AAA51592.	
21	885	83.6	193	6 ABU7022	XX		
22	885	83.6	193	6 ABU1576	PT	Nucleic acids encoding interleukin-1-like polypeptides, useful for preventing and treating e.g. inflammation, asthma and psoriasis.	
23	885	83.6	193	6 ABU91030	PT		
24	885	83.6	193	6 ABU27351	XX		
25	885	83.6	193	6 ABU92546	PS	Claim 22; Fig 2; 143pp; English.	

CC An isolated nucleic acid molecule encoding an interleukin-1-like
 CC polypeptide (IL-1 β) that retains one or more activities of the peptide
 CC from which it is derived, such as the IL-1 β binding activity of a human
 CC interleukin-1 receptor antagonist-1 (hIL-1Ra) polypeptide, is new. The
 CC nucleic acids may be used in molecular engineering applications, e.g.
 CC hybridization assays and chromosome and gene mapping studies, for
 CC recombinantly producing the IL-1 β polypeptide or for producing gene
 CC knock out animals to study the role of the protein in metabolism and
 CC disease processes (conversely, gene therapy protocol may be used to
 CC supplement a patients production of the polypeptide or to rectify
 CC mutations that lead to the production of inactive peptides). The
 CC peptides produced may be used to screen for and produce modulators (e.g.
 CC antibodies) of IL-1 β protein expression and activity which may be used to
 CC treat disorders associated with inappropriate IL-1 β expression and
 CC activity, such as inflammatory disorders, asthma, arthritis,
 CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress
 CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
 CC psoriasis, graft versus host disease and/or inflammatory bowel disease,
 XX SQ Sequence 203 AA;

Query Match 100.0%; Score 1059; DB 3; Length 203;
 Best Local Similarity 100.0%; Pred. No. 2e-113;
 Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSALLILALVGAADVYKDDDKLAAANSALRGPKVNLNPKFKSIHDQDKVVLVDSG 60
 Db 1 MSALLILALVGAADVYKDDDKLAAANSALRGPKVNLNPKFKSIHDQDKVVLVDSG 60
 Qy 61 NLTAVPDKNYIREPEIFFALASSLSSAASEKGSPILLGVSKGFCYCDKQKQSHSLQL 120
 Db 61 NLTAVPDKNYIREPEIFFALASSLSSAASEKGSPILLGVSKGFCYCDKQKQSHSLQL 120
 Qy 121 KKEKLMKLAQKESARRPFFIFTRAQVGSWNMLSAAHPGWFCITSCNCNEPVGVTDKPEN 180
 Db 121 KKEKLMKLAQKESARRPFFIFTRAQVGSWNMLSAAHPGWFCITSCNCNEPVGVTDKPEN 180
 Qy 181 RKEIEFSFQPVCKAEMSPSEVSD 203
 Db 181 RKEIEFSFQPVCKAEMSPSEVSD 203

RESULT 2

AY95397

ID AAY95297 standard; protein; 192 AA.

AC AAY95297;

XX DT 12-SEP-2000 (first entry)

XX DE Human interleukin-1 zeta.

XX KW Interleukin-1 zeta; IL-1 zeta; human; therapy; inflammation; fever.

XX OS Homo sapiens.

XX WO200036108-A2.

XX PD 22-JUN-2000.

XX XX 14-DEC-1999; 99W0-US029549.

XX PR 14-DEC-1998; 98US-0112163P.

XX PR 10-NOV-1999; 99US-0164675P.

XX XX (IMMV) IMMUNEX CORP.

XX PT TDZ1, TDZ2, TDZ3 and their encoding proteins, useful as probes for
 PT identifying genes associated with diseases such as glaucoma, and insulin-
 PT dependent diabetes mellitus.

XX PS

Claim 10; Page 8; 87pp; English.

XX SQ Sequence 192 AA;

Query Match 85.6%; Score 906; DB 3; Length 192;
 Best Local Similarity 100.0%; Pred. No. 8.4e-96;
 Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 RGPVKVNLNPKFSIHDQDKVVLVDGNGLAVPDKNYIREPEIFFALASSLSSAEGK 92
 Db 22 RGPVKVNLNPKFSIHDQDKVVLVDGNGLAVPDKNYIREPEIFFALASSLSSAEGK 81
 Qy 93 PILGVSKGERFCYCDKQKQSHSLQLKKKEKLMKLAQKESARRPFFYRAQVGSWNML 152
 Db 82 PILGVSKGERFCYCDKQKQSHSLQLKKKEKLMKLAQKESARRPFFYRAQVGSWNML 141
 Qy 153 ESAAHPGWFCITSCNCNEPVGVTDKFENRKIEFSFQPVCKAEMSPSEVSD 203
 Db 142 ESAAHPGWFCITSCNCNEPVGVTDKFENRKIEFSFQPVCKAEMSPSEVSD 192

RESULT 3

AY95300

ID AAY95300 standard; protein; 197 AA.

AC AAY95300;

XX DT 12-SEP-2000 (first entry)

XX DE Human interleukin-1 zeta splice variant TDZ.2.

XX KW Interleukin-1 zeta; IL-1 zeta; splice variant; human; TDZ.2;

XX OS Homo sapiens.

XX WO200036108-A2.

XX PD 22-JUN-2000.

XX PR 14-DEC-1999; 99W0-US029549.

XX PR 14-DEC-1998; 98US-0112163P.

XX PR 10-NOV-1999; 99US-0164675P.

XX XX (IMMV) IMMUNEX CORP.

XX PT TDZ1, TDZ2, TDZ3 and their encoding proteins, useful as probes for
 PT identifying genes associated with diseases such as glaucoma, and insulin-
 PT dependent diabetes mellitus.

XX PS

Claim 10; Page 8; 87pp; English.

XX SQ Sequence 192 AA;

Query Match 85.6%; Score 906; DB 3; Length 192;
 Best Local Similarity 100.0%; Pred. No. 8.4e-96;
 Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 RGPVKVNLNPKFSIHDQDKVVLVDGNGLAVPDKNYIREPEIFFALASSLSSAEGK 92
 Db 22 RGPVKVNLNPKFSIHDQDKVVLVDGNGLAVPDKNYIREPEIFFALASSLSSAEGK 81
 Qy 93 PILGVSKGERFCYCDKQKQSHSLQLKKKEKLMKLAQKESARRPFFYRAQVGSWNML 152
 Db 82 PILGVSKGERFCYCDKQKQSHSLQLKKKEKLMKLAQKESARRPFFYRAQVGSWNML 141
 Qy 153 ESAAHPGWFCITSCNCNEPVGVTDKFENRKIEFSFQPVCKAEMSPSEVSD 203
 Db 142 ESAAHPGWFCITSCNCNEPVGVTDKFENRKIEFSFQPVCKAEMSPSEVSD 192

RESULT 3

AY95300

ID AAY95300 standard; protein; 197 AA.

AC AAY95300;

XX DT 12-SEP-2000 (first entry)

XX DE Human interleukin-1 zeta splice variant TDZ.2.

XX KW Interleukin-1 zeta; IL-1 zeta; splice variant; human; TDZ.2;

XX OS Homo sapiens.

XX WO200036108-A2.

XX PD 22-JUN-2000.

XX PR 14-DEC-1999; 99W0-US029549.

XX PR 14-DEC-1998; 98US-0112163P.

XX PR 10-NOV-1999; 99US-0164675P.

XX XX (IMMV) IMMUNEX CORP.

XX PT TDZ1, TDZ2, TDZ3 and their encoding proteins, useful as probes for
 PT identifying genes associated with diseases such as glaucoma, and insulin-
 PT dependent diabetes mellitus.

XX PS

Claim 10; Page 8; 87pp; English.

XX SQ Sequence 192 AA;

Query Match 85.6%; Score 906; DB 3; Length 192;
 Best Local Similarity 100.0%; Pred. No. 8.4e-96;
 Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 RGPVKVNLNPKFSIHDQDKVVLVDGNGLAVPDKNYIREPEIFFALASSLSSAEGK 92
 Db 22 RGPVKVNLNPKFSIHDQDKVVLVDGNGLAVPDKNYIREPEIFFALASSLSSAEGK 81
 Qy 93 PILGVSKGERFCYCDKQKQSHSLQLKKKEKLMKLAQKESARRPFFYRAQVGSWNML 152
 Db 82 PILGVSKGERFCYCDKQKQSHSLQLKKKEKLMKLAQKESARRPFFYRAQVGSWNML 141
 Qy 153 ESAAHPGWFCITSCNCNEPVGVTDKFENRKIEFSFQPVCKAEMSPSEVSD 203
 Db 142 ESAAHPGWFCITSCNCNEPVGVTDKFENRKIEFSFQPVCKAEMSPSEVSD 192

PA (IMMUN) IMMUNEX CORP.
 XX
 PI Sima JE, Smith DE, Born TL;
 XX
 DR WPI: 2000-442387/38.
 DR NPSDB; AAB2921.
 XX
 PT Isolated interleukin-1 (IL-1) zeta nucleic acids and splice variants
 TDZ1, TDZ2, TDZ3 and their encoding proteins, useful as probes for
 PT identifying genes associated with diseases such as glaucoma, and insulin-
 dependent diabetes mellitus.
 XX
 PS Claim 10; Page 11; 87pp; English.
 XX
 CC The present sequence is that of splice variant TDZ2 (testis-derived zeta
 variant) of human interleukin-1 zeta (IL-1 zeta). TDZ2 mRNA is generated
 from exons 1, 4, 5 and 6 of the IL-1 zeta locus, and the encoded protein
 is probably a functional IL-1 like molecule. TDZ2 mRNA is expressed most
 strongly in the testis and bone marrow. The invention is directed to
 novel, purified and isolated IL-1 zeta, its splice variants and Xrc2
 polypeptides (see AAB527/301), the nucleic acids (see AAB2918-22)
 encoding such polypeptides, processes for production of recombinant forms
 of such polypeptides, and their uses. The polypeptides can be used to
 study cellular processes such as immune regulation, cell proliferation,
 cell death, cell migration, cell-to-cell interaction and inflammatory
 responses, to identify proteins associated with IL-1 zeta, to screen for
 potential inhibitors, and to prepare antibodies. In particular, they can
 be used to activate and/or inhibit the activation of vascular endothelial
 cells and lymphocytes, induce and/or inhibit the induction of local
 tissue destruction and fever, inhibit and/or stimulate macrophages and
 vascular endothelial cells to produce IL-6, induce and/or inhibit the
 induction of prostaglandins, nitric oxide synthetase, and
 CC metalloprotease, and upregulate and/or inhibit the upregulation of
 CC molecules on the surface of vascular endothelial cells
 XX
 Sequence 197 AA;
 SQ
 Query Match 85.2%; Score 902; DB 3; Length 197;
 Best Local Similarity 91.5%; Pred. No. 2.5e-95;
 Matches 172; Conservative 4; Mismatches 6; Indels 6; Gaps 1;
 Qy 16 DKKDDDKLAAANALCARGPKVKLNPKESIHODHKVLVLDGSGNIAVPDKNYIRBI 75
 Db 16 DWKDEPO----CCLBGPVKVKLNPKFSIHODHKVLVLDGSGNIAVPDKNYIRBI 69
 Qy 76 PFKLASSSSAERKGSPILLGSKGEFLYCDKDKGSHPSQLKKERKLMKLAQKES 135
 Db 70 PFKLASSSSAERKGSPILLGSKGEFLYCDKDKGSHPSQLKKERKLMKLAQKES 129
 Qy 136 RRPFIYRAQGVSNMLESAAHPWFCTSCNCNEPVGVTDKFENRKHIEFSQPVCKAE 195
 Db 130 RRPFIYRAQGVSNMLESAAHPWFCTSCNCNEPVGVTDKFENRKHIEFSQPVCKAE 189
 Qy 195 MSPSEVSD 203
 Db 190 MSPSEVSD 197
 XX
 RESULT 4
 AAB85138
 ID AAB85138 standard; protein; 198 AA.
 XX
 AC AAB85138;
 XX
 DT 22-AUG-2001 (first entry)
 XX
 DE Interleukin-1 homologue (IL-1H4) mature polypeptide.
 XX
 KW Interleukin-1; IL-1H4; antiinflammatory; antibacterial; antiallergic;
 KW immunosuppressive; antipsoriatic; antiarthritic; cytoprotective; antiHIV;
 KW cerebroprotective; antiasthmatic; vasoconstrictor; vulnerary; osteoprotective;
 KW immunomimetic; antiarteriosclerotic; nootropic; neuroprotective;
 KW gene therapy; vaccine.

XX
 Homo sapiens.
 XX
 PN WO200140247-A1.
 XX
 PD 07-JUN-2001.
 XX
 PF 30-NOV-2000; 2000WO-US032521.
 XX
 PR 01-DEC-1999; 99US-00452140.
 XX
 PA (SMK) SMITHKLINE BEECHAM CORP.
 XX
 PI Kumar S, McDonnell PC, Young PR;
 XX
 DR WPI: 2001-389949/41.
 XX
 Novel Interleukin-1 homolog, IL-1H4, for treating chronic and acute
 PT inflammation, septicemia, autoimmune diseases, transplant rejection,
 PT graft versus host disease, stroke, ischemia, allergy and asthma.
 XX
 PS Claim 1; Page 29; 30pp; English.
 XX
 CC The invention provides an isolated interleukin-1 homologue, IL-1H4
 CC polypeptide. The IL-1H4 polypeptide can be expressed by standard
 recombinant methodology. The IL-1H4 polypeptide, polynucleotides and
 CC peptides are useful for treating chronic and acute inflammation,
 septicemia, autoimmune diseases (e.g., inflammatory bowel disease,
 CC psoriasis and arthritis) transplant rejection, graft versus host
 disease, infection, stroke, ischemia, acute respiratory disease syndrome,
 CC allergies, asthma, restenosis, brain injury, AIDS, bone diseases (e.g.,
 osteoporosis), cancer (e.g., lymphoproliferative disorders), congestive
 heart failure, atherosclerosis and Alzheimer's disease. The IL-1H4
 CC polynucleotides are useful as diagnostic reagents and for chromosome
 CC identification. The present sequence represents the IL-1H4 mature
 CC polypeptide.
 XX
 Sequence 198 AA;
 SQ
 Query Match 84.5%; Score 835; DB 4; Length 198;
 Best Local Similarity 100.0%; Pred. No. 1.6e-94;
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 35 PKVNLNPKFSIHODHKVLVLDGSGNIAVPDKNYIRPEIFFALASSLSSAAEKGSP 94
 Db 30 PKVNLNPKFSIHODHKVLVLDGSGNIAVPDKNYIRPEIFFALASSLSSAAEKGSP 89
 Qy 95 LIGVSKGEFLYCDKDKGSHPSQLKKERKLMKLAQKESARRPPIFRAQGVSNMLES 154
 Db 90 LIGVSKGEFLYCDKDKGSHPSQLKKERKLMKLAQKESARRPPIFRAQGVSNMLES 149
 Qy 155 AAHGWFCFTSCNCNEPVGVTDKFENRKHIEFSQPVCKAEWSPSE/SD 203
 Db 150 AAHGWFCFTSCNCNEPVGVTDKFENRKHIEFSQPVCKAEWSPSE/SD 198
 XX
 RESULT 5
 AAY96938
 ID AAY96938 standard; protein; 207 AA.
 XX
 AC AAY96938;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE Human IL-1 receptor antagonist 1 long.
 XX
 KW hIL1RA1L; human interleukin-1 receptor antagonist-1 long; IL-1Lp;
 KW osteoprotective; interleukin-1-like polypeptide; anti-inflammatory;
 KW anti-asthmatic; anti-arthritic; antimicrobial; respiratory; vaccine;
 KW anti-ischemic; dermatological; immunomodulatory; gastrointestinal;
 KW gene therapy.
 XX
 OS Homo sapiens.

XX
 XX
 PR 27-OCT-1998; 98US-00179614.
 XX
 XX
 PA (ZIMO) ZYMOGENETICS INC.
 XX
 PI West RR, Sheppard PO, Gao Z;
 XX
 DR WPI; 2000-350740/30.
 DR N-PSDB; AAA00210.
 XX
 PT Immunomodulatory interleukin-1 homolog zilla4 proteins, useful for
 PT treatment of e.g. arthritis, psoriasis, septic shock, graft-versus-host
 disease, leukemia.
 PS Claim 4; Fig 2; 88pp; English.
 XX
 CC The present sequence is the human interleukin (IL)-1 homolog zilla4
 CC protein. This protein contains a core structure of 12 beta-strands wound
 CC into a beta-barrel, with the beta-strands separated from each other by
 CC loops. The loops between these beta-strands are highly variable among the
 CC family members and are believed to be involved in receptor binding. The
 CC zilla4 proteins modulate inflammation and other immunological processes
 CC and are therefore useful for treatment of arthritis, psoriasis, septic
 CC shock, graft-versus-host disease and leukaemia. Other diseases that may
 CC be modulated by zilla4 proteins include cancer, anaemia, inflammatory
 CC bowel disease, acute and chronic neuropathologies, shock, respiratory
 CC disease syndrome, restenosis and acquired immune deficiency syndrome
 XX
 SQ Sequence 218 AA;

Query Match 84.5%; Score 895; DB 3; Length 218;
 Best Local Similarity 100.0%; Pred. No. 1.9e-94; Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 35 PKVKNLNPKKFSIHQDKHVVLVDSGNLIAPDKNYIREIFFALASSLSSAEGKSPI 94
 Db 50 PKVKNLNPKKFSIHQDKHVVLVDSGNLIAPDKNYIREIFFALASSLSSAEGKSPI 109

Oy 95 LGVSKGGERFLYCDKQGSHPSLQLKEKLMKLAQKESARRPFPYRAQGVSNMLES 154
 Db 110 LGVSKGGERFLYCDKQGSHPSLQLKEKLMKLAQKESARRPFPYRAQGVSNMLES 169

Oy 155 AAHPGWFCCTSNCNEPGVTDKFNKRKIEFSQPVCKAEMSPSEVD 203
 Db 170 AAHPGWFCCTSNCNEPGVTDKFNKRKIEFSQPVCKAEMSPSEVD 218

RESULT 7
 AAY91885
 ID AAY91885 standard; protein; 218 AA.
 XX
 AC AAY91885;
 XX
 DT 19-JUL-2000 (first entry)
 XX
 DE Primate interleukin-1 like molecule (IL-1-zeta) alternative sequence.
 XX
 KW Primate; interleukin-1 like; IL-1-zeta; systemic inflammation; fever;
 KW hypoglycemia; plasma iron; plasma zinc; acute liver response;
 KW plasma copper.
 XX
 OS Mammalia.

XX
 XX
 FH Key location/Qualifiers
 FT Domain 58. .64 /label= beta _strand_1
 FT Domain 69. .74 /label= beta _strand_2
 FT Domain 76. .80 /label= beta _strand_3
 FT Domain 91. .96 /label= beta _strand_4
 FT Binding-site 100. .106

FT /note= "forms a loop which is part of a primary binding segment to the IL-1 receptor type"
 FT Domain 107. .113 /label= beta _strand_5
 FT Domain 118. .126 /label= beta _strand_6
 PI /label= beta _strand_7
 FT Domain 131. .136 /label= beta _strand_7
 FT Domain 154. .161 /label= beta _strand_8
 FT Domain 163. .169 /label= beta _strand_9
 FT Domain 176. .180 /label= beta _strand_10
 FT Domain 185. .204 /label= beta _strand_11
 FT Domain 201. .204 /label= beta _strand_12
 XX
 PN WO200017363-A2.
 XX
 PD 30-MAR-2000.

XX
 PR 17-SEP-1998; 98US-0015696.
 XX
 PA (ISCB) SCHERING CORP.
 XX
 PI Timans JC;
 XX
 DR WPI; 2000-283588/24.
 DR N-PSDB; AAA08513.

XX
 PT New mammalian interleukin 1 like molecule, designated IL-1-zeta, useful
 PT for diagnostic and therapeutic purposes, comprises a 128 amino acid
 PT sequence.

XX
 PS Claim 1; Page 103-104; 110pp; English.

XX
 CC The present sequence is an alternative primate interleukin-1 like
 CC molecule, designated IL-1-zeta. The 12 beta strands indicated in the
 CC features table, fold into a beta-trefoil fold. The specification claims
 CC an isolated or recombinant polypeptide that: (a) specifically binds
 CC polyclonal antibodies generated against at least a 12 consecutive amino
 CC acid segment of IL-1-zeta (see AAY91884) or its allelic variant (see
 CC AAY91885); and (b) comprises at least one sequence selected from:
 CC AAY9186-903 or AAY9190-4. The preferred 12 consecutive amino acid
 CC segment is chosen from AAY91907-18 or AAY91919-21. IL-1-zeta is likely to
 CC play a role in systemic inflammatory reactions, such as fever,
 CC hypoglycemia, reduced plasma iron and zinc, the acute response of the
 CC liver, and increase plasma copper. IL-1-zeta binding compounds
 CC (comprising antigen binding sites) and IL-1-zeta polypeptides are also
 CC useful for both diagnostic and therapeutic purposes

XX
 SQ Sequence 218 AA;

Query Match 84.5%; Score 895; DB 3; Length 218;
 Best Local Similarity 100.0%; Pred. No. 1.9e-94; Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 35 PKVKNLNPKKFSIHQDKHVVLVDSGNLIAPDKNYIREIFFALASSLSSAEGKSPI 94
 Db 50 PKVKNLNPKKFSIHQDKHVVLVDSGNLIAPDKNYIREIFFALASSLSSAEGKSPI 109

Oy 95 LGVSKGGERFLYCDKQGSHPSLQLKEKLMKLAQKESARRPFPYRAQGVSNMLES 154
 Db 110 LGVSKGGERFLYCDKQGSHPSLQLKEKLMKLAQKESARRPFPYRAQGVSNMLES 169

Oy 155 AAHPGWFCCTSNCNEPGVTDKFNKRKIEFSQPVCKAEMSPSEVD 203
 Db 170 AAHPGWFCCTSNCNEPGVTDKFNKRKIEFSQPVCKAEMSPSEVD 218

RESULT 8

Db 110 IIGVSKGEFCIYCDKQKSHPSLQKKEKLMQKESARRPFFYRAQVGSWMLIES 169
 AAY95299
 ID AAY95299 standard; protein; 218 AA.

XX
 AC AAY95299;
 XX

DT 12-SEP-2000 (first entry)

XX Human interleukin-1 zeta splice variant TDZ.1.

XX Interleukin-1 zeta; IL-1 zeta; splice variant; human; TDZ.1; KW testis-derived zeta variant; therapy; inflammation; fever.

OS Homo sapiens.

XX WO20036108-A2.

XX PD 22-JUN-2000.

XX PT 14-DEC-1999; 99WO-US029549.

XX PR 14-DEC-1998; 98US-0112163P.

XX PR 10-NOV-1999; 99US-0164675P.

XX PA (IMMV) IMMUNEX CORP.

XX PT Sims JE, Smith DE, Born TL;

XX DR N-PSDB; AAA27920.

XX PS Claim 10; Page 11; 87pp; English.

CC The present sequence is that of splice variant TDZ.1 (testis-derived zeta variant) of human interleukin-1 zeta (IL-1 zeta). TDZ.1 mRNA is generated from exons 1, 2, 4, 5 and 6 of the IL-1 zeta locus, and the encoded protein is probably a functional IL-1 like molecule. TDZ.1 mRNA is expressed most strongly in the kidney, skeletal muscle, testis, prostate, ovary, colon, small intestine, liver, placenta, lung, tonsil, foetal liver, lymph node and bone marrow. The invention is directed to novel, purified and isolated IL-1 zeta, its splice variants and Xrc22 polypeptides (see AAY95297-301, the nucleic acids (see AAY21918-22) encoding such polypeptides, processes for production of recombinant forms of such polypeptides, and their uses. The polypeptides can be used to study cellular processes such as immune regulation, cell proliferation, cell death, cell migration, cell-to-cell interaction and inflammatory responses, to identify proteins associated with IL-1 zeta, to screen for potential inhibitors, and to prepare antibodies. In particular, they can be used to activate and/or inhibit the activation of vascular endothelial cells and lymphocytes, induce and/or inhibit the induction of local tissue destruction and fever, inhibit and/or stimulate macrophages and vascular endothelial cells to produce IL-6, induce and/or inhibit the induction of prostaglandins, nitric oxide synthetase, and metalloproteases, and upregulate and/or inhibit the upregulation of molecules on the surface of vascular endothelial cells

XX Sequence 218 AA;

Query Match 84.5%; Score 895; DB 3; Length 218;
 Best Local Similarity 100.0%; Pred. No. 1.9e-94; Mismatches 0; Indels 0; Gaps 0;
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SQ 35 PPKVNLNPKKFESIHDQDKHVVLVLDGSLIJIADVDKNYTRPFFALASSLSSAEGKSP 94
 Qy 50 PPKVNLNPKKFESIHDQDKHVVLVLDGSLIJIADVDKNYTRPFFALASSLSSAEGKSP 109
 Qy 95 IIGGVSKGEFCIYCDKQKSHPSLQLKKEKLMQKESARRPFFYRAQVGSWMLIES 154

Db 110 IIGVSKGEFCIYCDKQKSHPSLQKKEKLMQKESARRPFFYRAQVGSWMLIES 169
 AAY95290
 ID AAY95290 standard; protein; 218 AA.

XX
 AC AAY95290;
 XX

DT 31-OCT-2000 (first entry)

XX Human IL-1 receptor antagonist 1 V.

XX DE 22-DEC-1999; 99WO-US030720.

XX PT 23-DEC-1998; 98US-011430P.

XX PR 22-JAN-1999; 99US-011643P.

XX PR 13-APR-1999; 99US-012912P.

XX DA (GBT) GENENTECH INC.

XX PT Goddard A, Pan J;

XX DR WPI; 2000-452395/39.

XX DR N-PSDB; AAY51604.

CC Nucleic acids encoding interleukin-1-like polypeptides, useful for preventing and treating e.g. inflammation, asthma and psoriasis.

XX PS Claim 22; Fig 19; 143pp; English.

XX CC An isolated nucleic acid molecule encoding an interleukin-1-like polypeptide (IL-1 β) that retain one or more activities of the peptide from which it is derived, such as the IL-1 β R binding activity of a human interleukin-1 receptor antagonist-1 (IL-1Ra) polypeptide, is new. The nucleic acids may be used in molecular engineering applications, e.g. hybridization assays and chromosome and gene mapping studies, for recombinantly producing the IL-1 β polypeptide or for producing gene knock out animals to study the role of the protein in metabolism and disease processes. (conversely, gene therapy protocols may be used to supplement a patient's production of the polypeptide or to rectify mutations that lead to the production of inactive peptides). The peptides produced may be used to screen for and produce modulators (e.g. antibodies) of IL-1 β protein expression and activity which may be use to treat disorders associated with inappropriate IL-1 β expression and activity, such as inflammatory disorders, asthma, arthritis, osteoarthritis, sepsis, acute lung injury, adult respiratory distress syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease, psoriasis, graft versus host disease and/or inflammatory bowel disease

XX Sequence 218 AA;

Query Match 84.5%; Score 895; DB 3; Length 218;
 Best Local Similarity 100.0%; Pred. No. 1.9e-94; Mismatches 0; Indels 0; Gaps 0;
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAG68116	OS	Homo sapiens.
ID	XX	
AAG68116;	XX	
AC	FT	Location/Qualifiers
XX	FT	Key
DE	FT	1..20
DT	FT	Peptide
22-JAN-2002	FT	/note= "signal peptide"
(first entry)	FT	
XX	FT	20..21
DE	FT	21..218
Human interleukin 1 family protein SBQ ID NO:2.	FT	/note= "specifically claimed mature protein (AAB85138)"
XX	FT	
KW	Protein	
identification.	FT	
XX	Protein	
OS	XX	
Homo sapiens.	XX	
XX	XX	
PN	XX	
JP2001231578-A.	XX	
XX	XX	
PD	XX	
28-AUG-2001.	XX	
XX	XX	
PF	XX	
07-DEC-2000; 2000JP-00372864.	XX	
PR	XX	
09-DEC-1999; 99JP-00349780.	XX	
XX	XX	
PA	XX	
(KYOW) KYOWA HAKKO KOGYO KK.	XX	
XX	XX	
DR	XX	
N-PSDB; AAI71179.	XX	
XX	XX	
PT	XX	
An IL-1 family protein, used for the development of diagnostic and	XX	
PT	XX	
treatment agents.	XX	
PS	XX	
Claim 1; Page 30; 38pp; Japanese.	XX	
CC	CC	
CC	CC	
The present sequence represents a human interleukin 1 (IL-1) family	CC	
protein having a combining affinity to a receptor of a protein of human	CC	
IL-1 family higher than Tango-77. The protein is useful for the	CC	
development of diagnostic, treating and/or preventive agents for various	CC	
diseases	CC	
XX	CC	
Sequence 218 AA;	CC	
Query Match	84.5%	Score 895; DB 4; Length 218;
Best Local Similarity	100.0%	Pred. No. 1..9e-4; Mismatches 0; Indels 0; Gaps 0;
Matches	169;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	35	PKVKNLNPKFKSTHDQHKVLVIDSGNLIAVDPDKNYIRPEIFALASSLSSASAEGSPI 94
Db	50	PKVKNLNPKFKSFHDQHKVLVIDSGNLIAVDPDKNYIRPEIFALASSLSSASAEGSPI 109
Qy	95	LIGVSKGEFCLYCDKDGKQSHPSLQLKKEKLMKLAQKESARPPFYRAQGSMWLES 154
Db	110	LIGVSKGEFCLYCDKDGKQSHPSLQLKKEKLMKLAQKESARPPFYRAQGSMWLES 169
Qy	155	AHPGWFICTSNCNCEPVGVTDFKENRKHIESFQPVCKAEMSPSEVD 203
Db	170	AHPGWFICTSNCNCEPVGVTDFKENRKHIESFQPVCKAEMSPSEVD 218
RESULT 13		
ABB85136		
ID		
ABB85136 standard; protein; 218 AA.		
XX		
AC		
ABB85136;		
XX		
DE		
Interleukin-1 homologue (IL-1H4) polypeptide.		
XX		
DE		
Interleukin-1; IL-1H4; antiinflammatory; antibacterial; antiallergic;		
KW		
immunosuppressive; antipsoriatic; antiarthritic; cryostatic; antihIV;		
KW		
cerebroprotective; antiasthmatic; vasotropic; vulnerary; osteopathic;		
KW		
immunostimulant; antiarteriosclerotic; nontropic; neurotropic;		
KW		
gene therapy; vaccine.		
XX		
RESULT 14		
AY71084		
ID		
AY71084 standard; protein; 218 AA.		
XX		
AC		
AY71084;		
XX		
DE		
05-SEP-2000 (first entry)		
XX		
DE		
Human zilla4-E2000 variant protein.		
XX		
KW		
Human interleukin-1; IL-1; zilla4 protein; inflammation; arthritis;		

KW psoriasis; septic shock; graft-versus-host disease; leukaemia; cancer;
 KW anaemia; inflammatory bowel disease; acute neuropathology; shock;
 KW chronic neuropathology; respiratory disease syndrome; restenosis;
 KW acquired immune deficiency syndrome; AIDS; antiinflammatory; cytostatic;
 KW anti-arthritis; anti-psoriatic; antibacterial; immunosuppressive;
 KW anti-anemic; neuroprotective; vasotropics; variant;
 KW anti-human immunodeficiency virus; HIV.
 OS Homo sapiens.
 XX
 PN WO200024899-A2.
 XX
 PD 04-MAY-2000.
 XX
 PF 27-OCT-1999; 99WO-US025038.
 XX
 PR 27-OCT-1998; 98US-00179614.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PT West RR, Sheppard PO, Gao Z;
 XX
 DR WPI; 2000-350740/30.
 XX
 PT Immunomodulatory interleukin-1 homolog zilla4 proteins, useful for
 PT treatment of e.g. arthritis, psoriasis, septic shock, graft-versus-host
 disease, leukemia.
 XX
 PS Claim 3; Page: 88pp; English.
 CC
 CC zilla4 protein, consisting of Asp in place of Glu at position 200. The
 CC replacement of Glu (200) with Asp results in attenuation of pro-
 CC inflammatory activity of zilla4 protein. The zilla4 proteins modulate
 CC inflammation and other immunological processes and are therefore useful
 CC for treatment of arthritis, psoriasis, septic shock, graft-versus-host
 CC disease and leukaemia. Other diseases that may be modulated by zilla4
 CC proteins include cancer, anaemia, inflammatory bowel disease, acute and
 CC chronic neuropathologies, shock, respiratory disease syndrome, restenosis
 CC and acquired immune deficiency syndrome. Note: The present sequence is
 CC not shown in the specification but is derived from human zilla4 protein
 XX
 Sequence 218 AA;
 SQ
 Query Match 84.2%; Score 892; DB 3; Length 218;
 Best Local Similarity 99.4%; Pred. No. 4.2e-94;
 Matches 168; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 35 PKVKNLNPCKPSIHQDKHKLVLDSGNLTAVPDKNYIRPEIFFALASSLSSAEGKSPI 94
 Db 50 PKVKNLNPCKPSIHQDKHKLVLDSGNLTAVPDKNYIRPEIFFALASSLSSAEGKSPI 109
 QY 95 LLGVSKGGERCLYCDKDGOSHPSIQLKEKLMKLAQESARPPFIRRAQVGSWNMBS 154
 Db 110 LLGVSKGGERCLYCDKDGOSHPSIQLKEKLMKLAQESARPPFIRRAQVGSWNMBS 169
 QY 155 AAHKGWFICTSNCNEPVGVTDKENRKIEFSQPVCAEMSPSEVD 203
 Db 170 AAHKGWFICTSNCNEPVGVTDKENRKIEFSQPVCAEMSPSEVD 218

RESULT 15
 AAY70933
 ID AAY70933. standard; protein; 218 AA.
 AC
 XX
 DT 05-SEP-2000 (first entry)
 XX
 DB Human zilla4-B200K variant protein.
 XX
 KW Human interleukin-1; IL-1; zilla4 protein; inflammation; arthritis;

KW psoriasis; septic shock; graft-versus-host disease; leukaemia; cancer;
 KW anaemia; inflammatory bowel disease; acute neuropathology; shock;
 KW chronic neuropathology; respiratory disease syndrome; restenosis;
 KW acquired immune deficiency syndrome; AIDS; antiinflammatory; cytostatic;
 KW anti-arthritis; anti-psoriatic; antibacterial; immunosuppressive;
 KW anti-anemic; neuroprotective; vasotropics;
 KW anti-human immunodeficiency virus; HIV.
 OS Homo sapiens.
 XX
 PN WO200024899-A2.
 XX
 PD 04-MAY-2000.
 XX
 PF 27-OCT-1999; 99WO-US025038.
 XX
 PR 27-OCT-1998; 98US-00179614.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PT West RR, Sheppard PO, Gao Z;
 XX
 DR WPI; 2000-350740/30.
 DR N-18DB; AAD0212.
 XX
 PT Immunomodulatory interleukin-1 homolog zilla4 proteins, useful for
 PT treatment of e.g. arthritis, psoriasis, septic shock, graft-versus-host
 disease, leukemia.
 XX
 PS Claim 8; Page 77-78; 88pp; English.
 XX
 CC
 CC zilla4 protein designated zilla4-B200K. The replacement of Glu (200) with
 CC Lys results in change in activity from agonist to antagonist. The zilla4
 CC proteins modulate inflammation and other immunological processes and are
 CC therefore useful for treatment of arthritis, psoriasis, septic shock,
 CC graft-versus-host disease and leukaemia. Other diseases that may be
 CC modulated by zilla4 proteins include cancer, anaemia, inflammatory bowel
 CC disease, acute and chronic neuropathologies, shock, respiratory disease
 CC syndrome, restenosis and acquired immune deficiency syndrome
 XX
 Sequence 218 AA;
 SQ
 Query Match 84.1%; Score 891; DB 3; Length 218;
 Best Local Similarity 99.4%; Pred. No. 5.4e-94;
 Matches 168; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 35 PKVKNLNPCKPSIHQDKHKLVLDSGNLTAVPDKNYIRPEIFFALASSLSSAEGKSPI 94
 Db 50 PKVKNLNPCKPSIHQDKHKLVLDSGNLTAVPDKNYIRPEIFFALASSLSSAEGKSPI 109
 QY 95 LLGVSKGGERCLYCDKDGOSHPSIQLKEKLMKLAQESARPPFIRRAQVGSWNMBS 154
 Db 110 LLGVSKGGERCLYCDKDGOSHPSIQLKEKLMKLAQESARPPFIRRAQVGSWNMBS 169
 QY 155 AAHKGWFICTSNCNEPVGVTDKENRKIEFSQPVCAEMSPSEVD 203
 Db 170 AAHKGWFICTSNCNEPVGVTDKENRKIEFSQPVCAEMSPSEVD 218

Search completed: September 9, 2004, 13:25:12
 Job time : 127 sec

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 9, 2004, 13:19:49 ; Search time 117 Seconds

(without alignments)
547.438 Million cell updates/sec

Title: US-09-869-566-5

Perfect score: 1059

Sequence: 1 NSALLTIALVGAAGADVYKDD.....TEFSFQPVCKAEMSPEVSD 203

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : SPTRIMBL 25;*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp Rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteria:*

17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1	173	16.3	159	11	Q8CGA1	Q8gal mus musculu	Q91wp7 mus musculu
2	158.5	15.0	159	4	Q96GD6	Q96gd6 homo sapien	Q8uug3 oncorhynchu
3	152.5	14.4	267	13	Q73Q99	Q96gd6 gallus gall	Q9yqgd3 oncorhynchu
4	151	14.3	176	6	Q9BEHO	Q9beh0 canis famili	Q9tik1 tursiops tr
5	150	14.0	277	13	Q9GM24	Q9gm24 turiosps tr	Q8wir2 delphinaptere
6	148	14.0	177	6	Q9DDP2	Q9ddp2 cyprinus ca	Q89gw7 paralichthys
7	148	14.0	177	6	Q86R8B	Q86r8 macaca fasc	Q98sg5 scophthalmu
8	145.5	13.7	272	13	Q8AKV9	Q8akv9 carassius a	Q98sg5 scophthalmu
9	141	13.3	176	6	Q9GK22	Q9gk22 canis famili	Q9tik1 tursiops tr
10	137.5	13.0	272	13	Q9DP3	Q9dp3 cyprinus ca	Q9tik1 tursiops tr
11	136	12.8	273	13	Q7T056	Q7t056 brachydanio	Q9tik1 tursiops tr
12	129.5	12.2	276	13	Q9PM18	Q9pm18 cyprinus ca	Q9tik1 tursiops tr
13	129.5	12.2	276	13	Q9AKV8	Q9akv8 carassius a	Q9tik1 tursiops tr
14	128.5	12.1	238	13	Q2082	Q2082 sus scrofa	Q9tik1 tursiops tr
15	128	12.1	267	6	Q29082	Q29082 sus scrofa	Q9tik1 tursiops tr
16	11.8	6	211	6	Q7Y541	Q7y541 sus scrofa	Q9tik1 tursiops tr

DR InterPro: IPR008996; Cytok_III-like.
 DR InterPro: IPR000975; Interleukin_1.
 DR Pfam: PF00340; IL1; 1.
 DR ProDom: PDO05336; Interleukin_1; 1.
 DR SMART: SM00125; IL1; 1.
 DR PROSITE: PS00253; INTERLEUKIN_1; 1.
 KW Receptor.
 SQ SEQUENCE 176 AA; 19922 MW; 8486CA54A240212B CRC64;
 Query Match 14.3%; Score 151; DB 6; Length 176;
 Best Local Similarity 28.4%; Pred. No. 3.6e-07;
 Matches 46; Conservative 27; Mismatches 76; Indels 10; Gaps 6;
 Score 14.3%;保守性 27%; 错配 76%; 缺口 10%; 空白 6%;
 QY 32 CRGPKVKNLPKKKSHDQPHKVLDGSGNLTAVPDKNYRPEIFFALASSLSSASAEGK 91
 DB 25 CRPLGKPCRMQAFRIWDVNQTKFVLRNNQVLA---GVLQGS-NTKLEBKLDVVPVPEH 79
 QY 92 SPILLGVSKGEFLYCDKDKQKOSHSLQKKEKLMKLAQKESARRPFFYRAQVGSMW 151
 DB 80 A-VFLGIGHGKGLCLACVKSGDETR--LOEAVNITDLSKNDQDKR-FPFLSDSGPTT 135
 QY 152 LESAHHPGWFCITCSNCNCNEPVGVTDKFENRKHI-EFSFQ 189
 DB 136 FESIACPGWFLCTLEADPVSITNREAMMVTFKEYFO 174
 Q9GMZ4 PRELIMINARY; PRT; 177 AA.
 ID Q9GMZ4 PRELIMINARY; PRT; 177 AA.
 AC Q9GMZ4: 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DB Interleukin 1 beta 2-2.
 GN IL-1_BETA 2.
 OS Cyprinus carpio (Common carp).
 OC Bukaryota; Metazoa; Chordata; Craniata; vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cyprinus.
 OX NCBI_TAXID=7962;
 RN [1]
 RA SEQUENCE FROM N.A.
 RT Engelsma M.Y., Stet R.J.M., Verburg-van Kemenade L.B.M.; Cloning and sequencing of two carp interleukin 1 beta 2 complementary DNA; Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RT DR EMBL; AJ01031; CAC19888.1; .
 RT DR HSSP; P01584; 211B.
 RT DR GO; GO:0005576; C:extracellular; IEA.
 RT DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
 RT DR GO; GO:0006935; P:immune response; IEA.
 RT DR GO; GO:0006934; P:inflammatory response; IEA.
 RT DR InterPro; IPR008996; Cytok_III_like.
 RT DR InterPro; IPR003502; IL1_propep.
 RT DR InterPro; IPR000975; Interleukin_1.
 RT DR Pfam; PF00340; IL1; 1.
 RT DR SMART; SM00125; IL1; 1.
 RT DR PROSITE; PS00253; INTERLEUKIN_1; 1.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21109087; PubMed=1182153;
 RA Inoue Y., Itou T., Jimbo T., Syouji Y., Ueda K., Sakai T.;
 RT "molecular cloning and functional expression of bottle-nosed dolphin
 RT (Tursiops truncatus) interleukin-1 receptor antagonist.";
 RT RL Var. Immunol. Immunopathol. 78:131-141(2001).
 DR AB031868; BAB18061; -.
 DR HSSP; P18510; ILRA.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:001549; F:interleukin-1 receptor binding; IEA.
 DR GO; GO:004872; P:receptor activity; IEA.
 DR GO; GO:0006935; P:immune response; IEA.
 DR InterPro; IPR008996; Cytok_III_like.
 DR InterPro; IPR000975; Interleukin_1.
 DR Pfam; PF00340; IL1; 1.
 DR ProDom; PDO05336; Interleukin_1; 1.
 DR SMART; SM00125; IL1; 1.
 DR PROSITE; PS00253; INTERLEUKIN_1; 1.
 KW Receptor.
 SQ SEQUENCE 177 AA; 19923 MW; 6FD19A06C09B131B CRC64;
 Query Match 14.2%; Score 150; DB 6; Length 177;
 Best Local Similarity 28.4%; Pred. No. 4.6e-07;
 Matches 46; Conservative 21; Mismatches 53; Indels 42; Gaps 6;
 Score 14.2%;保守性 21%; 错配 53%; 缺口 42%; 空白 6%;
 QY 45 FSIHQDQHKLVLDSGNLIA-----VPDKNYRPEIFFALASSLSSASA 88
 DB 38 FRTMDVNOKTFYLRNNOLVAGYQLOGPNTKLEKIDVVP---TEPHAMP--- 82
 QY 89 EKGSPLILGVSKGEFLYCDKDKQKOSHSLQKKEKLMKLAQKESARRPFFYRAQVG 148
 DB 83 -----LGIHGGKCLACVKSGDEI--KLGLPVNITDLSKEDKR-FAPFRSDSGP 132
 Q96GR8 PRELIMINARY; PRT; 177 AA.
 ID Q96GR8 PRELIMINARY; PRT; 177 AA.
 AC Q96GR8; 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DB IL-1 receptor antagonist.
 OS Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
 OX NCBI_TAXID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.

RESULT 8

Query Match 14.0%; Score 148; DB 6; Length 177;

Best Local Similarity 30.2%; Pred. No. 7; 4e-07;

Matches 42; Conservative 26; Mismatches 57; Indels 14; Gaps 7;

DR 42 PRK--PSIHDQDKHVLVDGSMILAVPDKNTR-PEIFFALASSAEEKSPILLG 97

DR 32 PSKMQAFYRIVDVKNQKTYLNNQLVAA---GYLQGPNA--NLKEKIDVPIPHAF-LFLG 84

DR 98 VSKGBFCLYCDKDGKQSHPSLQKKEKLMKLAQKESARRPPIFYRAQVGSWM 157

DR 85 INGGKMCILSCVVSQSGDETR-LQLEAVNITDLSKRNQDKR-FAFVRSDSGPTISFESAC 141

DR 158 PGMFICTSNCNCPVGVTD 176

DR 142 PGWFLCTAMEADOPVSLN 160

RESULT 9

Best Local Similarity 27.4%; Pred. No. 2.3e-06;

Matches 43; Conservative 31; Mismatches 66; Indels 17; Gaps 5;

DR 31 LCRGPKVKNLNPKKFPSIHDDQDKHVLVDGSMILAVPDKNTR-PEIFFALASSAEEK 90

DR 121 ICDKYKTKLVLVOSNKLNLNEDLNUKAVTILASGN-----LMLKLAQKESARRPPIFYRAQVGSWM 171

DR EMBL: AY18232; AAO24703.1; -

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0005955; P:immune response; IEA.

DR Interpro; IPR000975; Cytok_ILL_like.

DR Interpro; IPR000975; Interleukin_1.

DR SMART; SM00125; ILL_1.

DR PROSITE; PS00253; INTERLEUKIN_1; 1.

DR KW Receptor; PS00253; INTERLEUKIN_1; 1.

SQ SEQUENCE 177 AA; 19892 MW; FB7938A96BF360P CRC64;

Query Match 14.0%; Score 148; DB 6; Length 177;

Best Local Similarity 30.2%; Pred. No. 7; 4e-07;

Matches 42; Conservative 26; Mismatches 57; Indels 14; Gaps 7;

DR 42 PRK--PSIHDQDKHVLVDGSMILAVPDKNTR-PEIFFALASSAEEKSPILLG 97

DR 32 PSKMQAFYRIVDVKNQKTYLNNQLVAA---GYLQGPNA--NLKEKIDVPIPHAF-LFLG 84

DR 98 VSKGBFCLYCDKDGKQSHPSLQKKEKLMKLAQKESARRPPIFYRAQVGSWM 157

DR 85 INGGKMCILSCVVSQSGDETR-LQLEAVNITDLSKRNQDKR-FAFVRSDSGPTISFESAC 141

DR 158 PGMFICTSNCNCPVGVTD 176

DR 142 PGWFLCTAMEADOPVSLN 160

RESULT 10

Best Local Similarity 27.4%; Pred. No. 2.3e-06;

Matches 43; Conservative 31; Mismatches 66; Indels 17; Gaps 5;

DR 31 LCRGPKVKNLNPKKFPSIHDDQDKHVLVDGSMILAVPDKNTR-PEIFFALASSAEEK 90

DR 121 ICDKYKTKLVLVOSNKLNLNEDLNUKAVTILASGN-----LMLKLAQKESARRPPIFYRAQVGSWM 171

DR 91 GSPILIGVSKGFCLYCDKDGKQSHPSLQKKEK--LMLKLAQKESARRPPIFYRAQVGSWM 147

DR 172 GCPVCLASNSNLVYACTESGSS-PILLKEVSGQLNTIRKGDQNGYDSLFFRKETGT 230

DR 148 SNMLESAAHPCWFCITSCNCNEPVGV---TDKFFEN 180

DR 231 AYNTFESWKYPGWYSTAFDDWERVERMIVQVPTDRIN 267

DR 09GK2 PRELIMINARY; PRT; 176 AA.

DR 09GK2 ID 09GK2

DR AC 09GK2;

DR DT 01-MAR-2001 (TREMBrel. 16, Last sequence update)

DR DT 01-MAR-2001 (TREMBrel. 16, Last annotation update)

DR DE Interleukin-1 receptor antagonist.

DR OS Canis familiaris (Dog).

DR OC Barking; Metacida; Chordata; Craniata; Vertebrata; Euteleostomi;

DR OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

DR RN [1] NCBI_TAXID:9615;

DR SEQUENCE FROM N.A.

DR RX MEDLINE=21109092; PubMed=1182158;

DR RA Campbell S.B., Nasir L., Argyle D.J., Gault E.A., Duthie S.,

DR Bennett D.; "Cloning of canine IL-1ra, TNFR and TIM-2.";

DR RT Vet. Immunol. Immunopathol. 78:207-214(2001).

DR RL AAG3777.1; -

DR EMBL: AF216526;

DR HSSP; P18510; IL1R.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR Interpro; IPR000975; Interleukin_1.

DR Pfam; PF00340; ILL_1.

DR PRODOM; P00253; Interleukin_1; 1.

DR SMART; SM00125; ILL_1.

DR PROSITE; PS00253; INTERLEUKIN_1; 1.

DR KW Receptor; PS00253; INTERLEUKIN_1; 1.

SQ SEQUENCE 176 AA; 19938 MW; 8486CA54A254206B CRC64;

Query Match 13.3%; Score 141; DB 6; Length 176;

Best Local Similarity 28.3%; Pred. No. 3.7e-06;

Matches 45; Conservative 27; Mismatches 77; Indels 10; Gaps 6;

DR 32 CRGPVKVNLNPKKFPSIHDDQDKHVLVDGSMILAVPDKNTR-PEIFFALASSAEEK 91

DR 25 CRPLGKRCRMOAFRIVDVKNQKTYLNNQLVAA---GYLQGPNA--NLKEKIDVPIPHAF-LFLG 79

DR 92 SPILLGSKGERFLYCDKDGKQSHPSLQKKEKLMKLAQKESARRPPIFYRAQVGSWM 151

DR :80 A-VFLGIGHGGKLUCLACVSGDBTR-LQLEAVNITDLSKRNQDKR-FTFILSDGPTTS 135

DR 152 LESAHHPCWFCITSCNCNEPVGVTDKRENKRI-EFSQ 189

DR 136 FESACGFWFLCTAMEADOPVSLNREPEAMVTKFVQ 174

RESULT 11

Best Local Similarity 27.4%; Pred. No. 2.3e-06;

Matches 43; Conservative 31; Mismatches 66; Indels 17; Gaps 5;

DR 31 LCRGPKVKNLNPKKFPSIHDDQDKHVLVDGSMILAVPDKNTR-PEIFFALASSAEEK 90

DR 121 ICDKYKTKLVLVOSNKLNLNEDLNUKAVTILASGN-----LMLKLAQKESARRPPIFYRAQVGSWM 171

DR 91 GSPILIGVSKGFCLYCDKDGKQSHPSLQKKEK--LMLKLAQKESARRPPIFYRAQVGSWM 147

DR 172 GCPVCLASNSNLVYACTESGSS-PILLKEVSGQLNTIRKGDQNGYDSLFFRKETGT 230

DR 148 SNMLESAAHPCWFCITSCNCNEPVGV---TDKFFEN 180

DR 231 AYNTFESWKYPGWYSTAFDDWERVERMIVQVPTDRIN 267

DR 09DDF3 PRELIMINARY; PRT; 272 AA.

DR 09DDF3 ID 09DDF3

DR AC 09DDF3;

DR DT 01-MAR-2001 (TREMBrel. 16, Last sequence update)

DR DT 01-MAR-2001 (TREMBrel. 16, Last annotation update)

SQ SEQUENCE 272 AA; 30721 MW; A91E57D729770E13 CRC64;

Query Match 13.7%; Score 145.5; DB 13; Length 272;

QY 27 ANSALCRGPKVNLNPKKFESIHDDQHVLVLDGSLIAVDP--KVNIRPEIFFALASSL 84
 Db 107 ANGELCDATPVQSYDCK--LQDKEKAJLQPHFELKALHLKDKLBRVFCMSFVQG 163
 QY 85 SASAKRGSPPTLGLVSKGERFLYCK-DKDKGOSHPSIQLKKERKLMKLAQKESARRPIFIYR 143
 Db 164 DDSDDK-IPPTLIGKGKNLYLSCVMKD--DTPTQL--EDVDPPSYPRKDMEKKRFVFYK 217
 QY 144 AQGVSNMMLESAABPGWFICTSCNCNEPV 172
 Db 218 TEIKNRVERFESALYENWYISTSQABQPKV 246

Search completed: September 9, 2004, 13:27:43
Job time : 120 secs

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RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:200318623; PubMed=10860666;
 RA Busfield S.J., Comack C.A., Yu G., Chickering T.W., Smutko J.S., Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.; RT "Identification and gene organization of three novel members of the IL-1 family on human chromosome 2.;"
 RT Genomics 66:213-216 (2000).
 RL
 CC --!- FUNCTION: Function as an agonist of NF-kappa B activation through the orphan IL-1-receptor-related protein 2. Could constitute part of an independent signaling system analogous to interleukin-1 receptor type I (IL-1RI), that is present in epithelial barriers and takes part in local inflammatory response.
 CC --!- SUBCELLULAR LOCATION: Secreted.
 CC --!- TISSUE SPECIFICITY: Highly expressed in tissues containing epithelial cells: skin, lung, stomach and esophagus. In skin is expressed only in keratinocytes but not in fibroblast, endothelial cells or melanocytes. Up-regulated in lesional psoriasis skin.
 CC --!- INDUCTION: By TNF-alpha and by IFN-gamma in keratinocytes.
 CC --!- SIMILARITY: Belongs to the IL-1 family.
 CC
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 CC
 CC
 CC EMBL; AR20042; AAF69288.1; -.
 DR EMBL; AR206696; AAG35670.1; -.
 DR HSSP; P18510; I1IN; IL1F9.
 DR Genew; HGNC:15741; IL1F9.
 DR MMW; 605542; -.
 DR GO; GO:007267; P-cell-cell signaling; TAS.
 DR InterPro; IPR008986; Cytok_ILLike.
 DR InterPro; IPR00975; InterLeukin_1.
 DR Pfam; PF00340; I1I; 1.
 DR ProDom; P002536; InterLeukin_1.
 DR SMART; SMO025; I1I; 1.
 DR PROSITE; PS00253; INTERLEUKIN_1; FALSE_NEG.
 KW Cytokine; Multigene family.
 SQ SEQUENCE 169 AA; 18721 MW; F00A9243706F4154 CRC64;
 Query Match 21.7%; Score 229.5; DB 1; Length 169;
 Best Local Similarity 35.0%; Pred. No. 1.2a-14;
 Matches 56; Conservative 29; Mismatches 62; Indels 13; Gaps 5;
 QY 19 DDDDKLAANSALCRGPKVKNLNPKFSTHDQDHKVLVIDSGNIALAVPDKNYRPEIFFA 78
 Db 7 DADGGGRAYQQSMCK-----PTGTTINDLQWVPTQGNQVAVPRSDSUTPVTAV 58
 QY 79 LASSLSSASA-E-KSPILLGVSKGFBFLCDKGQSHSSLQKKEKLMKLAQKESARR 137
 Db 59 ITCKYPEALBGRGSDPIYLGQNPEMCLYCEKVSEQ-P-ILQLQEOKIMDLYGOPEPV-K 115
 QY 138 PFTYRAQGWSWNMLESAHPGWFICTSCNCNEPGVTK 177
 Db 116 PFLYRAKTRGRTSTLSEVAPPDWFIASS-KRDQDILSE 154
 RESULT 3
 I1F6_HUMAN STANDARD; PRT; 158 AA.
 ID I1F6_HUMAN; STANDARD; PRT; 158 AA.
 AC Q9HHA7;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Interleukin-1 family member 6 (IL-1F6) (Interleukin-1 epsilon) (IL-1 epsilon) (Pill epsilon).
 DE
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:20092888; PubMed=10625660;
 RA Smith D.E., Renshaw B.R., Ketcham R.R., Kubin M., Garka K.E., Sims J.E.;
 RT "Four new members expand the IL-1 superfamily.;"
 RL J. Biol. Chem. 275:1168-1175 (2000).
 CC --!- SUBCELLULAR LOCATION: Secreted (Potential).
 CC --!- TISSUE SPECIFICITY: Expressed in immune system and fetal brain, but not in other tissues tested or in multiple hematopoietic cell lines.
 CC --!- MISCELLANEOUS: Binding analysis failed to detect interaction with multiple IL1R family members.
 CC --!- SIMILARITY: Belongs to the IL-1 family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AR20181; AAF25211.1; -.
 DR HSSP; P18501; I1R.
 DR Genew; HGNC:15562; IL1F6.
 DR MMW; 605509; -.
 DR GO; GO:0005516; C:extracellular; NAS.
 DR GO; GO:0005449; F:interleukin-1 receptor binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR008986; Cytok_ILLike.
 DR InterPro; IPR00975; InterLeukin_1.
 DR Pfam; PF00340; I1I; 1.
 DR ProDom; P002536; InterLeukin_1.
 DR SMART; SMO0125; I1I; 1.
 DR PROSITE; PS00253; INTERLEUKIN_1; FALSE_NEG.
 KW Cytokine; Multigene family.
 SQ SEQUENCE 158 AA; 17684 MW; 469AC84306B0E280 CRC64;
 Query Match 19.7%; Score 209; DB 1; Length 158;
 Best Local Similarity 36.7%; Pred. No. 9.3e-13;
 Matches 54; Conservative 26; Mismatches 61; Indels 6; Gaps 4;
 QY 42 PKKFSIHDDHKVVLVIDSGNIALAVPDKNYRPEIFFALAS--SLSAACKGSPILLGSV 99
 Db 10 PQOQSIQDINHRVWVLQQTLLAVPRKORMSP-VTIANLISCRAVTELEKDRGKPIYLG 68
 QY 100 KGEFLCYDDKGQSHSPRLQKKEKLMKLAQKESARRPFFRAQWSWNMLESAAFG 159
 Db 69 GLNLICLMAKVGDO--PFLQLKEKMDIMLYQNEPEPV-FSFLFVHSQSCRNSTFESVAPFG 125
 QY 160 WFICTSNCNEPGVTDPEFENRHF 186
 Db 126 WFTAVSSPGCPLITDQSLGKANTDF 152
 RESULT 4
 I1F6_MOUSE
 ID I1F8_MOUSE; STANDARD; PRT; 183 AA.
 AC Q96Z6; Q8RA61;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Interleukin-1 family member 8 (IL-1F8).
 GN IL1F8 OR IL1E OR FILE.
 OC Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBi_TAXID=9606;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE:20092888; PubMed=10625660;
 RA Smith D.E., Renshaw B.R., Ketcham R.R., Kubin M., Garka K.E., Sims J.E.;
 RT "Four new members expand the IL-1 superfamily.;"
 RL J. Biol. Chem. 275:1168-1175 (2000).
 CC --!- SUBCELLULAR LOCATION: Secreted (Potential).
 CC --!- TISSUE SPECIFICITY: Expressed in immune system and fetal brain, but not in other tissues tested or in multiple hematopoietic cell lines.
 CC --!- MISCELLANEOUS: Binding analysis failed to detect interaction with multiple IL1R family members.
 CC --!- SIMILARITY: Belongs to the IL-1 family.
 CC
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 CC
 DR EMBL; AR20181; AAF25211.1; -.
 DR HSSP; P18501; I1R.
 DR Genew; HGNC:15562; IL1F6.
 DR MMW; 605509; -.
 DR GO; GO:0005516; C:extracellular; NAS.
 DR GO; GO:0005449; F:interleukin-1 receptor binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR008986; Cytok_ILLike.
 DR InterPro; IPR00975; InterLeukin_1.
 DR Pfam; PF00340; I1I; 1.
 DR ProDom; P002536; InterLeukin_1.
 DR SMART; SMO0125; I1I; 1.
 DR PROSITE; PS00253; INTERLEUKIN_1; FALSE_NEG.
 KW Cytokine; Multigene family.
 SQ SEQUENCE 158 AA; 17684 MW; 469AC84306B0E280 CRC64;
 Query Match 19.7%; Score 209; DB 1; Length 158;
 Best Local Similarity 36.7%; Pred. No. 9.3e-13;
 Matches 54; Conservative 26; Mismatches 61; Indels 6; Gaps 4;
 QY 42 PKKFSIHDDHKVVLVIDSGNIALAVPDKNYRPEIFFALAS--SLSAACKGSPILLGSV 99
 Db 10 PQOQSIQDINHRVWVLQQTLLAVPRKORMSP-VTIANLISCRAVTELEKDRGKPIYLG 68
 QY 100 KGEFLCYDDKGQSHSPRLQKKEKLMKLAQKESARRPFFRAQWSWNMLESAAFG 159
 Db 69 GLNLICLMAKVGDO--PFLQLKEKMDIMLYQNEPEPV-FSFLFVHSQSCRNSTFESVAPFG 125
 QY 160 WFICTSNCNEPGVTDPEFENRHF 186
 Db 126 WFTAVSSPGCPLITDQSLGKANTDF 152

OX NCBI_TAXID=10090; RN [1] SEQUENCE FROM N.A. RP STRAIN-Swiss Webster / NIH; RX MEDLINE=21988051; PubMed=11991723; RT "Genomic organization of the interleukin-1 locus."; RL Genomics 79:726-733 (2002). RP SEQUENCE FROM N.A. RN STRAIN=C57BL/6J; TISSUE=Tongue; RX MEDLINE=21085660; PubMed=11217851; RT Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., Fujita M., Garibaldi M., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Suzuki H., Toyooka K., Wang K.H., Weitz C., Witteker C., Wilming L., Wynnshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsukii S., RA Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; RT Nature 409:685-690 (2001). RL NATURE 409:685-690 (2001); CC -I- SUBCELLULAR LOCATION: Secreted (Potential). CC -I- SIMILARITY: Belongs to the IL-1 family. CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch). CC ----- CC EMBL: AY071842; AAL67152.1; ALT_INIT. CC DR EMBL; AK09787; BAB26505.1; -. CC DR InterPro; IPR00896; Cytok_III like. CC DR InterPro; IPR000975; Interleukin_1. CC DR MGI; MGI:1916927; IILf8. CC DR Pfam; PF00340; III; 1. CC DR prodom; PDO02536; Interleukin_1; 1. CC DR SMART; SM0125; III; 1. CC DR PROSITE; PS00253; INTERLEUKIN_1; 1. CC KW Cytokine; Multigene family. CC SEQUENCE 183 AA; 20878 MW; A3ACE339FB96F02F CRC64; CC Query Match 18.8%; Score 199; DB 1; Length 183; CC Best Local Similarity 33.3%; Pred. No. 9.8e-12; CC Matches 42; Conservative 53; Indels 4; Gaps 3; CC ----- CC 41. NPKKFSIHDQDKVULDSGNLIAVDPDKYIREPIFFAL-SSLSASAEGSPILIGVS 99 CC 34 SPRYRVHDQSQQMVLGNTLAVPASNNKVKVILSIACRDTFQDVKGALVFIGIK 93 CC 34 SPRYRVHDQSQQMVLGNTLAVPASNNKVKVILSIACRDTFQDVKGALVFIGIK 93 CC 100 KGERPLCYDKDKQKOSHPSIQLKCKLMKLAOKESARRPPIFYRAQGWNMLESAAHPG 159 CC 94 NRMILGFCVEMEGK--PTQLKEVDIMLYKERK-AQAKFLYHIGESTSVFQSVLPG 150 CC 160 WFICTS 165 CC 151 WFATTS 156

11P5_MOUSE STANDARD; PRT; 156 AA. ID 11P5_MOUSE STANDARD; PRT; 156 AA. AC 09QYY1; Q9UG2; DT 28-FEB-2003 (Rel. 41; Created) DT 28-FEB-2003 (Rel. 41; Last sequence update) DT 28-FEB-2003 (Rel. 41; Last annotation update) DE Interleukin 1 family member 5 (IL-1F5) (Interleukin-1-like protein 1) (IL-1 delta) (Interleukin-1-like protein 1) (Interleukin-1-like protein 1) (IL-1F5) (Interleukin-1-like protein 1) (IL-1F5) (Interleukin-1 homolog 3) (IL-1H3). DE IL1F5 OR F11D OR IL1HY1 OR IL1H3. OS Mus musculus (Mouse). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Nematoda; Actinopterygii; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. OC ----- RN [1] SEQUENCE FROM N.A. RP STRAIN=C57BL/6J; PubMed=11466363; RX MEDLINE=21159532; PubMed=11466363; RA Debets R., Timans J.C., Homet B., Zurawski S., Sana T.R., Lo S., Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F., RA Kasteler R.A.; Edwards G., Clifford T., Menon S., Bazan J.F., RA Barton J.L., Herbst R., Bosiso D., Higgins L., Nicklin M.J.H.; RA Griswold D.B., Capper E.A., Tal-Singer R., Weils G.I., Doyle M.L., RA Young P.R.; "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function as an antagonist and agonist of NF- κ B activation through the orphan IL-1 receptor-related protein 2.", RT orphan IL-1 receptor-related protein 2., RT cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities.; RT Eur. J. Immunol. 167:1440-1446 (2001). RL J. Immunol. 167:1440-1446 (2001). RN [2] SEQUENCE FROM N.A. RP STRAIN=C57BL/6J; PubMed=11093146; RX MEDLINE=20454521; PubMed=11093146; RA Barton J.L., Herbst R., Bosiso D., Higgins L., Nicklin M.J.H.; RA Griswold D.B., Capper E.A., Tal-Singer R., Weils G.I., Doyle M.L., RA Young P.R.; "Identification and initial characterization of four novel members of the interleukin-1 family.", RT "Identification and initial characterization of four novel members of the interleukin-1 family.", RT J. Biol. Chem. 275:10308-10314 (2000). RL J. Biol. Chem. 275:10308-10314 (2000). RN [4] SEQUENCE FROM N.A. RP STRAIN=C57BL/6J; TISSUE=Stomach, and Tongue; RX MEDLINE=21085660; PubMed=11217851; RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochi H., RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M., RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., RA Sasaki H., Sato K., Schoenbach C., Saya T., Shibata Y., Storch K.-F., RA Wynnshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohotsukii S., RA Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; RT Nature 409:685-690 (2001). CC -I- FUNCTION: Is a highly and a specific antagonist of the IL-1 receptor-related protein 2-mediated response to interleukin 1 family member 9 (IL1F9). Could constitute part of an independent signaling system analogous to interleukin-1 alpha (IL-1 α), beta (IL-1 β) receptor agonist and interleukin-1 receptor type I (IL-1R α), that is present in epithelial barriers and takes part in local inflammatory response (BY similarity). CC ----- CC

CC -!- TISSUE SPECIFICITY: Highly abundant in embryonic tissue and tissues containing epithelial cells.

CC CC -!- SIMILARITY: Belongs to the IL-1 family.

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CC CC EMBL; AF230378; AAF91275.1; -.

CC CC EMBL; AF230941; BAB26471.1; -.

CC CC EMBL; AK008977; BAB26002.1; -.

CC CC EMBL; AU250429; CAB59831.1; ALT_INIT.

CC CC EMBL; AF200495; AAF69251.1; -.

CC CC HSSP; P18510; IL1R.

DR MGD; MG1:1859325; IL1F5.

DR InterPro; IPR008986; Cytok IL1-like.

DR InterPro; IPR000975; InterLeukin_1.

DR Pfam; PF00340; IL1; 1.

DR ProDom; PD002536; Interleukin_1; 1.

DR SMART; SN0125; IL1.

DR PROSITE; PS0053; INTERLEUKIN_1; 1.

DR CYCOKINE; Multigene family.

FT SEQUENCE 156 AA; 17136 MW; A4D1EE2F93CF77A7 CRC64;

KW Best Local Similarity 35.1%; PRed. No. 4.2e-11;

Matches 53; Conservative 24; Mismatches 51; Indels 23; Gaps 6;

Query Match 18.1%; Score 191.5; DB 1; Length 156;

28 NSALCRGPKVKNLNPKKFSIHQDHKVULVDSGNLIA--VFDKNVIRPEIFFFALASSLSS 85

Db 5 SGALC-----ERIKDSALKVLYHNQNLLAGHHAEKVKGESIVPNRAID 52

QY 86 ASAEKGSPILGVSKQKBFCLYCDKQKGQSHPSLQLKKEKML-AAQKESARRPFIYRA 144

Db 53 ASL--SPVILGVQGQSCLSGCTKG--FILKLEPVNIMELYLGAKES--KSFTFIRR 104

QY 145 QVGSKMLLSAHAPGWFICTSNCNCPVGT 175

Db 105 DMGLTSSPESAAVPGWFLCTSPEADQPVRLT 135

RESULT 6

ID TIIF5_HUMAN STANDARD; PRT; 155 AA.

AC Q9D8H0; DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, last sequence update)

DT 10-OCT-2003 (Rel. 42, last annotation update)

DR Interleukin 5 family member 5 (IL-1F5) (Interleukin-1 delta) (IL-1 delta) (IL-1 delta) (Interleukin-1-like protein 1) (IL-1I)

DE (Interleukin-1 HY1) (IL-1HY1) (Interleukin-1 receptor antagonist homolog 1) (IL-1ra homolog 1) (IL-1 related protein 3) (IL-1RP3).

GN IL1F5 OR FILD OR IL1HY1 OR IL1I OR IL1RP3.

OS Homo Sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. OC NCBI_TaxId=9606;

RN SEQUENCE FROM N.A.

RC MEDLINE:20092888; PubMed=10625560;

RX RX MEDLINE=99443727; PubMed=10512743;

RA Mulero J.J., Pace A.M., Neikken S.T., Loeb D.B., Correa T.R.,

RA Drmanic R., Ford J.E.,

RA "ILHY1: a novel interleukin-1 receptor antagonist gene.";

RT Biochem. Biophys. Res. Commun. 263:702-706(1999).

RA [3];

RC TISSUE=Placenta;

RC SEQUENCE FROM N.A.

RA MEDLINE=20545212; PubMed=11093146;

RA Barron J.L., Herbst R., Bosisio D., Higgins L., Nicklin M.J.H.,

RT "A tissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-1ra, IL-1 β and IL-1 δ antagonist activities.";

RT Bur. J. Immunol. 30:3299-3308(2000).

RN [4]

RR SEQUENCE FROM N.A.

RA MEDLINE=21359532; PubMed=11466363;

RA Debets R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo S.,

RA Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,

RA Kastlein R.A.;

RT "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function as an antagonist and agonist of NF- κ B activation through the orphan IL-1 receptor-related protein 2.,";

RT J. Immunol. 167:1440-1446(2001).

RA [5]

RR SEQUENCE FROM N.A.

RA MEDLINE=20318623; PubMed=10860666;

RA Busfield S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S.,

RA Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.R.;

RT "Identification and gene organization of three novel members of the IL-1 family on human chromosome 2";

RT Genomics 66:213-216(2000).

RR [6]

RR SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RC MEDLINE=22389257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Grouse L.H.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Sculier G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaeffer C.F., Blat N.K.,

RA Hopkins R.F., Jordon H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soare M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villanueva D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Heitton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickey M.C.,

RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,

RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smailus D.E.,

RA Schinner A., Schein J.E., Jones S.J.M., Marra M.A.,

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: Is a highly and a specific antagonist of the IL-1 homolog 1 (IL-1ra homolog 1) (IL-1 related protein 3) (IL-1RP3).

CC "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";

CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: Is a highly and a specific antagonist of the IL-1 receptor-related protein 2-mediated response to interleukin 1 family member 9 (IL1F9). Could constitute part of an independent signaling system analogous to interleukin-1 alpha (IL-1A), beta (IL-1B) receptor agonist and interleukin-1 receptor type I (IL-1R1), that is present in epithelial barriers and takes part in local inflammatory response.

CC -!- TISSUE SPECIFICITY: Predominantly expressed in keratinocytes but also in fibroblasts, endothelial cells or melanocytes. Detected also in the spleen, brain leukocyte and macrophage cell types.

CC Increased in lesional psoriasis skin.

CC -!- INDUCTION: By phorbol ester (PMA) and lypopolysaccharide (LPS) treatment in macrophage cell line.

CC -!- SIMILARITY: Belongs to the IL-1 family.

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RX MEDLINE=21085660; PubMed=11217851;
 RA Kawaji J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsukawa H., Ashburner M., Batalov S., Caravati T.,
 RA Fleischmann M., Gaasterland T., Gibbs C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsumoto Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubach F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordt P., Ring B., Ringwald M., Rodriguez J., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibaoka Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynnshaw-Boruta A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -!- TISSUE SPECIFICITY: Highly expressed in embryonic tissue and in
 CC tissues containing epithelial cells.
 CC -!- MISCELLANEOUS: Binding analysis failed to detect interaction with
 CC multiple ILR family members.
 CC -!- SIMILARITY: Belongs to the IL-1 family.
 CC
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 or send an email to license@abb-sib.ch).
 CC
 DR SEQUENCE FROM N.A. (ISOFORM 1).
 DR STRAIN=SWISS;
 RX MEDLINE=9131673; PubMed=1830498;
 RA Matsushime H., Rousset M.F., Matsushima K., Hishinuma A., Sherr C.J.;
 RT "Cloning and expression of murine interleukin-1 receptor antagonist
 in macrophages stimulated by colony-stimulating factor 1.;"
 RL Blood 78:616-623 (1991).
 RN [3]
 DR SEQUENCE FROM N.A. (ISOFORM 1).
 DR STRAIN=SWISS;
 RX MEDLINE=9271931; PubMed=8003626;
 RA Zahedi K.A., Uhlar C.M., Rits M., Prada A.E., Whitehead A.S.;
 RT "The mouse interleukin 1 receptor antagonist protein: gene structure
 and regulation in vitro.;"
 RL Cytokine 6:1-9 (1994).
 RN [4]
 DR SEQUENCE FROM N.A. (ISOFORM 2).
 DR STRAIN=FVB X DBA/1 LACJ;
 RX MEDLINE=98209157; PubMed=9550387;
 RA Gabay C., Porter B., Fantuzzi G., Arend W.P.;
 RT "Mouse IL-1 receptor antagonist isoforms: complementary DNA cloning
 and protein expression of intracellular isoform and tissue
 distribution of secreted and intracellular IL-1 receptor antagonist in
 vivo";
 RL J. Immunol. 159:5905-5913 (1997).
 RN [5]
 DR SEQUENCE OF 7-178 FROM N.A.
 RX MEDLINE=91271363; PubMed=1828896;
 RA Eisenberg S.P., Brewer M.T., Verderber E., Heindl P.,
 RA Brandhuber B.J., Thompson R.C.;
 RT "Interleukin 1 receptor antagonist is a member of the interleukin 1
 gene family: evolution of a cytokine control mechanism.;"
 RL Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236 (1991).
 RN [6]
 DR SEQUENCE OF 23-178 FROM N.A.
 RX MEDLINE=92037824; PubMed=1834470;
 RA Shuck M.E., Bessau T.E., Tracey D.E., Bienkowski M.J.;
 RT "Cloning, heterologous expression and characterization of murine
 interleukin 1 receptor antagonist protein.;"
 RL Eur. J. Immunol. 21:2775-2780 (1991).
 CC -!- FUNCTION: Inhibits the activity of IL-1 by binding to its
 receptor. Has no IL-1 like activity.
 CC -!- SUBCELLULAR LOCATION: Secreted (Isoform 1). Cytoplasmic (isoform
 CC 2).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=p25085-1; Sequence=displayed;
 CC Name2;
 CC IsoId=p25085-2; Sequence=displayed;
 CC
 RESULT 9
 ILIX_MOUSE STANDARD; PRT; 178 AA.
 ID ILIX_MOUSE STANDARD; PRT; 178 AA.
 AC P25085; 070207;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)

CC or send an email to license@ibb-sib.ch).

CC

DR EMBL; M74254; AAA39309; 1; -. DR EMBL; M6404; AAA39277; 1; -. DR EMBL; I32838; AAAX20576; 1; -. DR EMBL; AF001795; AAC1251; 1; -. DR EMBL; M57525; AAA39278; 1; -. DR EMBL; M63100; AAAX39310; 1; -. DR EMBL; S64082; AAB20265; 1; -. DR PIR; A44610; A44610. DR HSSP; P18510; ILRA. DR MGD; MGI; 95347; ILRN. DR InterPro; IPR005996; Cytok_ILL_like. DR InterPro; IPR005975; Interleukin_1. DR ProDom; PDO02536; Interleukin_1. DR SMART; SM00125; ILI; 1. DR PROSITE; PS00253; INTERLEUKIN_1; 1. DR KW GLYCOPROTEIN; Signal; Alternative splicing. DR FT SIGNAL; 1; 158 DR FT CHAIN; 27; 178 DR FT DISULFID; 92; 142 DR FT CARBOPT; 110; 21 DR FT VARSPIC; 1; 21 DR SQ SEQUENCE; 178 AA; 20274 MW; 84AA002A3119C024 CRC64;

Query Match Best Local Similarity 31.1%; Score 167; DB 1; Length 178; Matches 51; Conservative 26; Mismatches 75; Indels 12; Gaps 7;

Qy 28 NSALCRGKVKUNPKPKSIHPODKHVKVILVDSGNCNLIAVDPDKYIR-BIEFLASSUSA 86 Db 22 SEACRPGSKRPKCMQARPIWNTQKTYLRRNQIA---GLQGNI-I-KLEEKIDMV 75

Qy 87 SAEKGSPILLGVSKGEGFLYCKDKKGQSHPSLQLKKERKLMLKAQKESARRPPIFYRAQV 146 Db 76 P10LHS-VFLGTHGKGKLCLSKAQSAGDPI---KQLEENVNTDLSKNEKEEDR-FTFIRSEK 131

Qy 147 GSNNMLLESAAH-PGWFICTSCNNCMEPVGVTDKFENRKH-T-EFQRQ 189 Db 132 GPTTSFESAACPGWFLCTLEADRPVSLNTPSBEPLIVTKFVFFQ 175

RESULT 10

LI1A MOUSE ID T1FA MOUSE STANDARD; PRT; 152 AA.

AC Q8R459; DT 28-FEB-2003 (Rel. 41, Created) DT 10-OCT-2003 (Rel. 41, Last sequence update) DE Interleukin 1 family member 10 (IL-1F10).

GN IL1F10. OS Mus musculus (Mouse). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. OK NCBI_TAXID=10090; RN [1]

RP SSEQUENCE FROM N.A. / NIH; MEDLINE=21988051; PubMed=11991723; CC Taylor S.L., Renshaw B.R., Garka K.E., Smith D.E., Sims J.E., RT "Genomic organization of the interleukin-1 locus."; RL Genomics 79:726-733 (2002).

CC -I- FUNCTION: Binds soluble IL-1 receptor type 1 (By similarity). CC -I- SUBCELLULAR LOCATION: Secreted (By similarity). CC -I- SIMILARITY: Belongs to the IL-1 family.

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CC

DR MGD; MGI; 265254; IL1F10. DR InterPro; IPR005996; Cytok_ILL_like. DR InterPro; IPR005975; Interleukin_1. DR Pfam; PF00340; ILI; 1. DR ProDom; PDO02536; Interleukin_1. DR SMART; SM00125; Interleukin_1; 1. DR PROSITE; PS00253; INTERLEUKIN_1; FALSE_NEG. DR KW Cytokine; Multigene family. DR SQ SEQUENCE; 152 AA; 1707 MW; 9AD03EB0C3C6LD8A CRC64;

Query Match Best Local Similarity 15.6%; Score 165.5; DB 1; Length 152; Matches 49; Conservative 33; Mismatches 72; Indels 7; Gaps 4;

Qy 45 FSIHDPDKHVLYTDGNS-LIAVPDKNYIRPIFFALASSUSA 86 Db 10 YIKDAHQKALYTRNGNGLLGDPSDMSNSPEKVCILPNRGLDRSK--VPFLGMGQGSC 66

Qy 104 CUYCDKDKGQSHPSLQLKEKUMKLAAQKESARRPPIFYRAQVGSNNMLESAAHCPWEIF 163 Db 67 CLACVKTR--EGPLLOLDVNEIDLYKGEGQTR-FTFORSILGSAFRLEAACPGWFLC 123

Qy 164 TSCNCNEFVGVDKFENRKH-EFSPQ 189 Db 124 GAAEPQQPVQLKESEPSTHTEFYFE 149

RESULT 11

LI1X_HUMAN ID LI1X_HUMAN STANDARD; PRT; 177 AA.

AC P18510; Q14628; Q96G06; Q9UPC0; DT 01-NOV-1990 (Rel. 16, Created) DT 01-NOV-1990 (Rel. 16, Last sequence update) DT 15-MAR-2004 (Rel. 43, Last annotation update) DE Interleukin-1 receptor antagonist protein precursor (IL-1ra) (ICIL-1RA) (IL-1RN). DE (IL-1RN).

GN OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cetartiodactyla; Homo. OC NCBI_TAXID=9606; RN [1]

RP SSEQUENCE FROM N.A. (ISOFORM 1). RX MEDLINE=903220867; PubMed=2139180; RA Carter D.B., Deibel M.R. Jr., Dunn C.J., Tomich C.S.C., Laborde A.L., RA Slichter J.L., Berger A.E., Blenkowski M.J., Sun F.F., McEwan R.N., RA Harris P.K.W., Yem A.W., Waszak G.A., Chosay J.G., Sieu L.C., RA Hardee M.W., Zurcher-Neely H.A., Reardon I.M., Heinrikson R.L., RA Truesdell S.E., Shelly J.A., Bessalou T.E., Taylor B.M., Tracey D.E.; RA "Purification, cloning, expression and biological characterization of an interleukin-1 receptor antagonist protein."; RL Nature 344:633-638(1990). RN [2]

RP SSEQUENCE FROM N.A. (ISOFORM 1). RX MEDLINE=90136921; PubMed=2137701; RA Eisenberg S.P., Evans R.J., Arend W.P., Verderber E., Brewer M.T., RA Hannum C.H., Thompson R.C.; RA Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P., RT "Primary structure and functional expression from complementary DNA of a human interleukin-1 receptor antagonist."; RL Nature 343:341-346(1990). RN [3]

RP SSEQUENCE FROM N.A. (ISOFORM 1). RX MEDLINE=91271363; PubMed=1828996; RA Eisenberg S.P., Thompson R.C., Brandhuber B.J., Thompson R.C.; RA "Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family: evolution of a cytokine control mechanism.";

RL PROC. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
 RN [4]
 R P SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=92338323; PubMed=1365987;
 RA Leonard A., Gorman P., Carrier M., Griffiths S., Scotney H.,
 RA Sheer D., Solari R.,
 RT "Cloning and chromosome mapping of the human interleukin-1 receptor
 RT antagonist gene.;"
 RN [5]
 R P SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
 RX MEDLINE=97146044; PubMed=8993991;
 RA Jenkins J.X., Drong R.F., Shuck M.E., Bienkowski M.J., Slightom J.L.,
 RA Arend W.P., Smith M.F. Jr.;
 RT "Intracellular IL-1 receptor antagonist promoter: cell type-specific
 RT and inducible regulatory regions.;"
 RL J. Immunol. 158:748-755(1997).
 RN [6]
 R P SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=91219436; PubMed=1827201;
 RA Hackl S., Martin G., van Le L., Morris J., Peace A., Bigler C.F.,
 RA Jaffe G.J., Hammerberg C., Sporn S.A., Fong S., Arend W.P., Ralph P.;
 RT "cDNA cloning of an intracellular form of the human interleukin 1
 RT receptor antagonist associated with epithelium.;"
 RL Proc. Natl. Acad. Sci. U.S.A. 88:3681-3685(1991).
 RN [7]
 R P SEQUENCE FROM N.A. (ISOFORM 3).
 RX MEDLINE=9535865; PubMed=7629520;
 RA Muzio M., Potentarutti N., Sirioni M., Poli G., De Gioia L.,
 RA Introna M., Mantovani A., Colletta F.;
 RT "Cloning and characterization of a new isoform of the interleukin 1
 RT receptor antagonist.;"
 RL J. Exp. Med. 182:623-628(1995).
 RN [8]
 R P SEQUENCE FROM N.A. (ISOFORM 2).
 RA Rider M.J., Carrington D.P., Hastings N.C., Ahearn M.O.,
 RA Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 RN [9]
 R P SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Pancreas;
 RX MEDLINE=22388175; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,
 RA Aitschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Blatchko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M., Bonaldo F., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prage C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faley J., Heaton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boutpard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimmwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krawinkel M.I., Skalsta U., Smailus D.B.,
 RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.;"
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [10]
 R P SEQUENCE OF 26-45.
 RX MEDLINE=90136920; PubMed=2137200;
 RA Haimov C.H., Wilcox C.J., Arend W.P., Joslin F.G., Driggs D.J.,
 RA Heindel P.L., Armes L.G., Sommer A., Eisenberg S.P., Thompson R.C.;
 RT "Interleukin-1 receptor antagonist activity of a human interleukin-1
 inhibitor.;"
 RL Nature 343:336-340(1990).
 RN [11]
 R P SEQUENCE OF 26-52.
 RX MEDLINE=90354444; PubMed=2143761;

RA Bienkowski M.J., Bessalu T.E., Berger A.E., Tressell S.E.,
 RA Shelly J.A., Laborde A.L., Zurich-Neely H.A., Reardon I.M.,
 RA Heinkson R.L., Chosay J.G., Tracey D.E.;
 RT "Purification and characterization of interleukin 1 receptor level
 RT antagonist proteins from THP-1 cells.;"
 RL J. Biol. Chem. 265:14505-14511(1990).
 RN [12]
 R P SEQUENCE OF 35-177 FROM N.A. (ISOFORM 4).
 RX MEDLINE=98183404; PubMed=9514884;
 RA Weisbach L., Tran K., Colquhoun S.A., Champlaud M.F., Towle C.A.;
 RT "Detection of an interleukin-1 intracellular receptor antagonist mRNA
 RT variant.;"
 RL Biochem. Biophys. Res. Commun. 244:91-95(1998).
 RN [13]
 R P STRUCTURE BY NMR.
 RX MEDLINE=92297633; PubMed=1534997;
 RA Stockman B.J., Scanill T.A., Roy M., Ulrich E.L., Strakalaitis N.A.,
 RA Brunner D.P., Yem A.W., Deibel M.R. Jr.;
 RT "Secondary structure and topology of interleukin-1 receptor
 RT antagonist protein determined by heteronuclear three-dimensional NMR
 RT spectroscopy.;"
 RL Biochemistry 31:5237-5244(1992).
 RN [14]
 R P STRUCTURE BY NMR.
 RX MEDLINE=94320651; PubMed=8045306;
 RA Stockman B.J., Scanill T.A., Strakalaitis N.A., Brunner D.P.,
 RA Yem A.W., Deibel M.R. Jr.;
 RT "Solution structure of human interleukin-1 receptor antagonist
 RT protein.;"
 RL FEBS Lett. 349:7-9-83(1994).
 RN [15]
 R P X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=94230368; PubMed=8175703;
 RA Vigers G.P.A., Caffes P., Evans R.J., Thompson R.C., Eisenberg S.P.,
 RA Brandhuber B.J.;
 RT "X-ray structure of interleukin-1 receptor antagonist at 2.0 Å
 RT resolution.;"
 RL J. Biol. Chem. 269:12874-12879(1994).
 RN [16]
 R P X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RX MEDLINE=95177072; PubMed=71867645;
 RA Schreuder H.A., Rondeau J.M., Tardif C., Soffientini A., Sarubbi B.,
 RA Akeson A., Bowlin T.L., Yanofsky S., Barrett R.W.;
 RT "Refined crystal structure of the interleukin-1 receptor antagonist.
 RT Presence of a disulfide link and a cis-proline.;"
 RL Eur. J. Biochem. 227:838-847(1995).
 RN [17]
 R P X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 32-177 IN COMPLEX WITH IL1R.
 RX MEDLINE=97215904; PubMed=962194;
 RA Schreuder H., Tardif C., Trump-Kallmeyer S., Soffientini A.,
 RA Sarubbi B., Akeson A., Bowlin T., Yanofsky S., Barrett R.W.;
 RT "A new cytokine-receptor binding mode revealed by the crystal
 RT structure of the IL-1 receptor with an antagonist.;"
 RL Nature 386:94-200(1997).
 CC -1- FUNCTION: Inhibits the activity of IL-1 by binding to its
 CC receptor. Has no IL-1 like activity.
 CC -1- SUBCELLULAR LOCATION: Secreted (isoform 1). Cytoplasmic (isoforms
 CC 2, 3 and 4).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1;
 CC Ibold=PI8510-1; Sequence=Displayed;
 CC Name=2; Synonyms=ICIL-1ra;
 CC Ibold=PI8510-2; Sequence=VSP_002649;
 CC Name=3; Synonyms=ICIL-1ra type II;
 CC Ibold=PI8510-3; Sequence=VSP_002650;
 CC Name=4;
 CC Ibold=PI8510-4; Sequence=VSP_002651;
 CC -1- TISSUE SPECIFICITY: THE INTRACELLULAR FORM OF IL-1RA IS
 CC PREDOMINANTLY EXPRESSED IN EPITHELIAL CELLS.
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 CC -1- DATABASE: NAME=R&D Systems' cytokine source book; IIRN;
 CC WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=205".

RESULT 15

IL1X_CANFA

ID _IL1X_CANFA STANDARD; PRT; 176 AA.

AC Q9BEHO; Q9EKK2;

DT 15-MAR-2004 (Rel. 43, Last sequence update)

DT 15-MAR-2004 (Rel. 43, last annotation update)

DE Interleukin-1 receptor antagonist protein precursor (IL-1Ra) (IL-1RN)

DE (IRAP)

GN IL1RN.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OC NCBI_TaxID:9615;

RN [1]

RP SEQUENCE FROM N.A.

RA Shin I.-S., Youn H.-Y.;

RA RT "Molecular cloning of canine interleukin-1 receptor antagonist (IL-1Ra).";

RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA MEDLINE=21109092; PubMed=11182158;

RA Bennett D., Argyle D.J., Gault E.A., Duthie S.,

RA RT "Cloning of canine IL-1ra, TNFR and TIMP-2.";

RL Vet. Immunol. Immunopathol. 78:207-214 (2001).

CC -i- FUNCTION: Inhibits the activity of IL-1 by binding to its

CC receptor. Has no IL-1 like activity (By similarity).

CC -i- SUBCELLULAR LOCATION: Secreted.

CC -i- SIMILARITY: Belongs to the IL1 family.

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CC -----

DR EMBL; AF216326; AAG36777.1; -.

DR RSP; P18510; IL1R.

DR InterPro; IPR008996; Cytok IL1-like.

DR InterPro; IPR000575; Interleukin_1.

DR Pfam; PF00340; IL1_1.

DR PRODOM; PD002536; Interleukin_1; 1.

DR SMART; SM0125; IL1_1.

DR PROSITE; PS00253; INTERLEUKIN_1; 1.

DR KW Glycoprotein; Signal.

PT SIGNAL 1 25 POTENTIAL.

PT CHAIN 26 176 INTERLEUKIN-1 RECEPTOR ANTAGONIST

PT PROTEIN.

PT BY SIMILARITY.

PT N-LINKED (GLCNAC. . .) (POTENTIAL).

PT P -> L (IN REF. 2).

FT CONFLICT 109 155 CRC64;

FT CONFLICT 155 155 P -> L (IN REF. 2).

FT SEQUENCE 176 AA; 19922 MW; 8486CA54A24021B CRC64;

Query Match 14.3%; Score 151; DB 1; Length 176;

Best Local Similarity 28.9%; Pred. No. 3.3e-07; Mismatches 27; Indels 10; Gaps 6;

Matches 46; Conservative 76;

PT SIGNAL 1 25 POTENTIAL.

PT CHAIN 26 176 INTERLEUKIN-1 RECEPTOR ANTAGONIST

PT PROTEIN.

PT BY SIMILARITY.

PT N-LINKED (GLCNAC. . .) (POTENTIAL).

PT P -> L (IN REF. 2).

FT CONFLICT 109 155 CRC64;

FT CONFLICT 155 155 P -> L (IN REF. 2).

FT SEQUENCE 176 AA; 19922 MW; 8486CA54A24021B CRC64;

Db 136 FBSAACPGWFLCTALEADRPVSLTRPEAMWVTFQ 174

Search completed: September 9, 2004, 13:25:39

Job time : 24 SECs

GenCore version 5.1.6
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Om protein - protein search, using sw model

Run on: September 9, 2004, 13:20:54 ; Search time 40 Seconds
(without alignments)
488.172 Million cell updates/sec

Title: US-09-869-566-5

Perfect score: 1059

Sequence: 1 MSALLILALVGAADVKKD IEFSFOFVCKAEMSPESEVSD 203

Scoring table: Blosum62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PTR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	174.5	16.5	155	2 JCT7104	interleukin-1 receptor antagonist - human
2	157	15.8	178	2 A44610	C;Species: Homo sapiens (man)
3	161	15.0	180	2 A39386	C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
4	158.5	15.0	177	2 A30368	C;Accession: JCT7104
5	154.5	14.6	177	2 A54377	R;Mulero, J.J.; Pace, A.M.; Nelken, S.T.; Loeb, D.B.; Correa, T.R.; Drmanac, R.; Ford, J
6	146.5	13.8	178	2 C40956	Biotech. Biophys. Res. Commun. 283, 702-706, 1999
7	131.5	12.4	266	1 S23010	A;Title: IL1H1: A novel interleukin-1 receptor antagonist gene.
8	128	12.1	267	2 S38373	A;Reference number: JCT7104; MUID:99443727; PMID:10512743
9	121.5	11.5	267	1 JN0724	A;Accession: JCT7104
10	120.5	11.4	269	1 JN0724	A;Molecule type: mRNA
11	118	11.1	266	1 ICB01B	A;Residues: 1-155 <MUL>
12	98	9.3	269	1 ICB01B	A;Cross-References: GB:AF186094; NID:96049804; PID:AAF02757.1; PID:96049805
13	95.5	9.0	246	2 B25528	A;Gene: il1h1
14	92.5	8.7	268	1 A30584	A;Map position: 2q14
15	91	8.6	404	2 S34031	C;Keywords: macrophage
16	89.5	8.5	214	2 JCT564	Query Match 28 NSALCRGPVKVNLNPKKFSIHDDHKVLYLDSGNLIAVFDKNYRPEIFFALSSLSS 87
17	84	7.9	270	1 ICMS1	Best Local Similarity 32.0%; Prd. No: 4.7e-09; Matches 54; Conservative 18; Mismatches 48; Indels 49; Gaps 7;
18	83.5	7.9	776	2 S67053	Db 4 SGALC-----FRMKSALKVLYLHNNO-----LAGGLHACK 35
19	82.5	7.8	246	1 TRT1	QY 88 AEKG-----SPILLGVSKGFCLYCDOKKGQSHPSLQJKKEKUML-RAQ 131
20	82	7.7	513	2 T37806	Db 36 VIKGKEISVVPNRWLADASLSPVILGVQGSOCLSC---GVGQ-BPITLLEPVNIMLYIGA 92
21	81	7.6	320	2 A81434	QY 132 KESARRPFTYRAQVGSMNMLSAAHPMWFICTSNCNCPVGVTDKFN 180
22	81	7.6	914	2 R96592	Db 93 KES---KSFYFYRDMGLISSLSPESAYVPGWFLCTVPEADQPVRLQPN 139
23	80.5	7.6	246	1 TRT2	RESULT 2
24	80.5	7.6	845	2 T17291	A44510
25	78.5	7.4	244	2 F90419	interleukin-1 receptor antagonist precursor - mouse
26	78	7.4	1277	2 E70224	N;Alternate names: IL-1Ra
27	77	7.3	859	2 C87358	C;Species: Mus musculus (house mouse)
28	76.5	7.2	231	2 S59589	C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 16-Jul-1999
29	76.5	7.2	375	2 F70151	C;Accession: A44610

hypothetical protein
dynamin light chain
hypothetical protein
glucan 1,3-beta-1
cell wall binding
trypsin (EC 3.4.21)
trypsin (EC 3.4.21)
trypsin (EC 3.4.21)
AddPolyceramanno-he
homeobox and LIM d
hypothetical protein
interleukin-1 alpha
coat protein - ade
K-Cl cotransport p
hypothetical protein
phosphoribosylform

hypothetical protein
dynamin light chain
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AddPolyceramanno-he
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interleukin-1 alpha
coat protein - ade
K-Cl cotransport p
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phosphoribosylform

ALIGNMENTS

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 A;Molecule type: DNA
 A;Accession: 7-178 <EIS>
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 A;Experimental source: peritoneal macrophage, ICR strain
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 A;Residues: 1-178 <RE2>
 A;Cross-references: GB:L132838; NID:9487864; PIDN:AA20576.1; PID:9528978
 C;Genetics:
 A;Gene: IL-1rn
 A;Introns: 40/2; 70/1; 107/3
 C;Superfamily: interleukin-1
 C;Keywords: interleukin receptor
 F1-26/Domain: signal sequence #status predicted <SIG>
 F1-27/8/Product: interleukin-1 receptor antagonist #status predicted <MA2>
 Query Match 15.8%; Score 167; DB 2; Length 178;
 Best Local Similarity 31.1%; Pred. No. 2; g-e-08;
 Matches 51; Conservative 26; Mismatches 75; Indels 12; Gaps 7;
 QY 28 NSALCLRGPKVKNLNPKKTSIHDDQHKVLYLDGSGNLIAVYDPDKNTR-PEIFFALASSISSA
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RESULT 4
 A30368
 C;Species: Homo sapiens (man)
 C;Date: 07-Jun-1990 #sequence revision 07-Jun-1990 #text change 26-May-2000
 C;Accession: A40956; I37894; A10368; S08160; S08160; A37822
 R;Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson, P.; Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
 A;Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family:
 A;Reference number: A40956; MUID:91291363; PMID:1828896
 A;Accession: A40956
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-177 <LEN>
 A;Cross-references: ENBL:X64552; NID:931798; PIDN:CAA4832.1; PID:931799
 R;Carter, D.B.; Deibel Jr., M.R.; Dunn, C.J.; Tomich, C.S.C.; Laborde, A.L.; Slightom, J.J.G.; Sieu, L.C.; Hardee, M.M.; Zurcher-Neely, H.A.; Reardon, I.M.; Heinrikson, R.L.; Tripathi, J.; Exp. Med. 182, 623-628, 1995
 A;Title: Cloning and characterization of a new isoform of the interleukin 1 receptor antagonist
 A;Reference number: I37894; MUID:9355865; PMID:762520
 A;Accession: I37894
 A;Status: translated from GB/EMBL/DDBJ
 A;Cross-references: GB:X53296; NID:932578; PIDN:CAA37386.1; PID:932579
 A;Note: parts of this sequence, including the amino end of the mature protein, were confirmed by R;Eisenberg, S.P.; Evans, R.J.; Arend, W.P.; Verderber, E.; Brewer, M.T.; Hannum, C.H.; Nature 343, 341-346, 1990

A;Molecule type: mRNA
 A;Residues: 1-177 <G0>
 A;Cross-references: GB:D21832; NID:9425787; PIDN:BAA04860.1; PID:9452205
 C;Superfamily: interleukin-1
 C;Keywords: cytokine receptor; extracellular protein; glycoprotein
 F;1-25/Domain: signal sequence #status predicted <SIG>
 F;109/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 14 6%; Score 154.5; DB 2; Length 177;
 Best Local Similarity 27.0%; Pred. No. 4.2e-07;
 Matches 44; Conservative 23; Mismatches 51; Indels 45; Gaps 6;
 Qy 32 CRGPKVKNLNUKKFSIHDQDHKVILVLDGSNLLA-----VPDKYKIRPEI 75
 Db 25 CRPSKSPCRNMQAARRIWDVQKTYVRLNNQVLAGYQPNKALERIDVVP---LPQL 80
 Qy 76 FFALASSLSSASAECGSPILLGVSKGEBFLCYCDK---DKGQSHPSQLKKEKLMKLAQKE 133
 Db 81 LF-----LGIQSKLCLSCVSKGSDDKMLH---LEAVNITDGLKNE 118
 Qy 134 SARRPPIFYRAQVGSMMLLESAHPSWFLCTSCNCNEPVGVTD 176
 Db 119 QDKR-FTFIRNSNSGPTTFFESASCPCGWNFLCTALEADQPVSLTN 160
 RESULT 6
 C40956 interleukin-1 receptor antagonist precursor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 16-Jul-1999
 C;Accession: C40956
 R;Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; T
 Proc. Natl. Acad. Sci. U.S.A. 88, 5223-5236, 1991
 A;Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene
 A;Reference number: A40956; MUID:91271363; PMID:1828896
 A;Accession: C40955
 A;Status: preliminary
 A;Molecule type: DNA
 A;Cross-references: GB:M63101; NID:9204928; PIDN:AAA41434.1; PID:9204929
 C;Superfamily: interleukin-1
 C;Keywords: cytokine receptor
 Query Match 13 8%; Score 146.5; DB 2; Length 178;
 Best Local Similarity 26.6%; Pred. No. 2.4e-06;
 Matches 47; Conservative 23; Mismatches 58; Indels 49; Gaps 6;
 Qy 31 LCRGKPKVKNLNU-----PKK---FSIHQDHKVILVLDGSNLLA--- 64
 Db 3 ICRGYSHLISLILLFRSAGKAGPKRCKMQAFFRIMTQNQKTYVRLNNQVLAGYQ 62
 Qy 65 -----VPDKYKTYRPEFFALASSLSSASAECGSPILLGVSKGEBFLCYCDKDKGQSHPSLQ 119
 Db 63 GPNTKLEKIDMNPDF-----RNVLFLGIHGKLCLSCVSKGSDDT-KLQ 105
 Qy 120 LKKELKLMKLAQKESARRPPIFYRAQVGSMMLLESAHPSWFLCTSCNCNEPVGVTD 176
 Db 106 LEEVNITDLNKNKEBDR-FTFIRSBTGPTTSFESLACPGWNFLCTTLEADQPVSLTN 161
 RESULT 7
 S23010 interleukin-1 beta precursor - sheep
 N;Alternate names: hematopoietin-1; IL-1 beta
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C;Date: 08-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 15-Oct-1999
 C;Accession: S23010; S41027; S13022; B01246
 R;Sew, H.F.; Rothel, J.S.; David, M.J.; Wood, P.R.
 DNA Seq. 1, 423-426, 1991
 A;Title: Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA.
 A;Reference number: S23010; MUID:92119335; PMID:1840515
 A;Accession: S23010
 A;Molecule type: mRNA

A;Residues: 1-266 <SEQ>
 A;Cross-references: EMBL:X56972; NID:91808; PIDN:CAA40233.1; PID:91809
 A;Note: the sequence shown in Fig. 1 is inconsistent with that from Fig. 2 in having an addi-
 R;Sargan, D.R.
 submitted to the EMBL Data Library, May 1992
 A;Reference number: S43047
 A;Accession: S43047
 A;Molecule type: mRNA
 A;Residues: 1-13, 'C', 15-54, 'K', 56-63, 'A', 65-144, 'L', 146-266 <SAR>
 A;Cross-references: EMBL:X54796; NID:91273; PIDN:CAA38566.1; PID:91274
 R;Fiskerstrand, C.; Sargan, D.
 Nucleic Acids Res. 18, 7165, 1990
 A;Title: Nucleotide sequence of ovine interleukin-1 beta.
 A;Reference number: S13092; MUID:91088326; PMID:2263490
 A;Accession: S13092
 A;Molecule type: mRNA
 A;Residues: 1-13, 'C', 15-54, 'K', 56-61, 'S', 63, 'A', 65-144, 'L', 146-266 <FIS>
 A;Note: the authors translated the codon AGT for residue 62 as Arg
 R;Andrews, A.E.; Barcham, G.J.; Brandon, M.R.; Nash, A.D.
 Immunology 74, 453-460, 1991
 A;Title: Molecular cloning and characterization of ovine IL-1alpha and IL-1beta.
 A;Reference number: A61246; MUID:92120716; PMID:1769692
 A;Accession: B61246
 A;Molecule type: mRNA
 A;Residues: 1-144, 'L', 146-266 <AND>
 C;Species: This protein lacks a conventional signal sequence for protein export. Cleavage
 A;Cross-references: I
 C;Key: interleukin-1beta, unlike interleukin 1-alpha, is inactive.
 C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a
 C;Genetics:
 A;Gene: IL-1-beta
 C;Key:
 C;Superfamily: interleukin-1
 C;Key:
 F;114-266/Product: interleukin-1 beta #status predicted <MAT>
 Query Match 12.4% Score 131.5; DB 1; Length 266;
 Best Local Similarity 27.2%; Pred. No. 9.7e-05;
 Matches 44; Conservative 30; Mismatches 63; Indels 25; Gaps 8;
 Db 17 YKPPDDKU--AANASALCRGPKVKNLNPKKSIHDQHKVYLDSG--NIAVPKQV 70
 103 FERSDELICDAAQVSK--LQDDBQKSYLTDSPCVLKHLRQEM 149
 QY 71 RREIFFALASSLSSASAEGKSPILLGVSKGEFLYCDKDKGOSHPSIQLKEKLMKLA 130
 150 SR-EVVFQMF-SFVQGEERDKNTIVALGIRDQKNUYLSCVK-KDPT-PRQL--EEVDPKV 203
 QY 131 QKESARRPPIFYRAQVGWNMLMSAAHRCGWFLCTSCNCNEPV 172
 204 PPKRMKEMKRVFVYKTEIKNTVEFESVLYPNWYISTSQEEKPV 245
 RESULT 8
 S38373 interleukin-1 beta precursor - pig
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 20-May-1994 #sequence_revision 01-Dec-1995 #text_change 16-Jul-1999
 C;Accession: S38373
 R;Vandenbroucke, K.; Fiten, P.; Beuken, E.; Martens, E.; Janssen, A.; van Damme, J.; Opde-
 Bur, J. Biochem. 217, 45-52, 1993
 A;Title: Gene sequence, cDNA construction, expression in *Escherichia coli* and geneticall
 A;Reference number: S38373; MUID:94039070; PMID:8223584
 A;Accession: S38373
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-267 <VAN>
 A;Cross-references: EMBL:X74568; NID:9407999; PIDN:CAA52660.1; PID:9407900
 C;Genetics:
 A;Introns: 16/2; 33/3; 99/1; 154/1; 197/3
 C;Superfamily: interleukin-1
 Query Match 12.1% Score 128; DB 2; Length 267;
 Best Local Similarity 28.9% Pred. No. 0.00021; Length 267;

Matches 43; Conservative 28; Mismatches 66; Indels 12; Gaps 6;
 QY 27 ANSAICGGPKVNLNPKKFSIHDQHKVYLDSGNLIAVPD--KNTIREPFALLSSL 84
 Db 107 ANGFLCIDATPVQSVQDVCK--LQDKDEKALVLAGPHFLKALHLKGDLKREVFVFCMSFVQG 163
 QY 85 SASAEEKSSPILIGVSKGEFLYCDKDKGOSHPSIQLKEKLMKLAQKESARPPIFYR 143
 164 DBDDDK-IPVTLGIKGSNLVYSCVMKD--DTPTLQ--EDVDPKSYPKRDMEKRIVFY 217
 QY 144 AQGVSWMMLSEAHPGMFICTSNCNCNEPV 172
 Db 218 TEIKNRVFEFESALYPNWYISTSQAEQKPV 246
 RESULT 9
 JN0724 interleukin-1 beta precursor - pig
 N;Alternate names: hematopoietin-1; IL-1 beta
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 14-Jul-1994 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999
 C;Accession: JN0724
 R;Huether, M.J.; Lin, G.; Smith, D.M.; Murgaugh, M.P.; Molitor, T.W.
 Gene 129, 285-289, 1993
 A;Title: Cloning, sequencing and regulation of an mRNA encoding porcine interleukin-1 beta.
 A;Reference number: JN0724; MUID:93314975; PMID:8325511
 A;Molecule type: mRNA
 A;Accession: 1-267 <HUB>
 A;Cross-references: GB:MB6725; NID:9164607; PIDN:AAA2584.1; PID:9164608
 A;Cross-references: GB:MB6725; NID:9164607; PIDN:AAA2584.1; PID:9164608
 C;Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophage
 F;115-267/Product: interleukin-1 beta #status predicted <IL1>
 F;77/Binding site: myristate (Lys) (covalent) #status predicted
 Query Match 11.5% Score 121.5; DB 1; Length 267;
 Best Local Similarity 25.9%; Pred. No. 0.0004;
 Matches 44; Conservative 28; Mismatches 73; Indels 25; Gaps 7;
 Db 19 DDDDK--LAAANASALCRGPKVKNLNPKKFSIHDQHKVYLDSGNLIAV 65
 QY 86 DDDQKSIFFSFIREEEFILETCNDDFVQDANVQSMCK--LQDKDHKSLVLAGPMLKA 142
 QY 66 PD--KMYRPEFFFAASLSSASAEGKSPILLGVSKGEFLYCDKDKGOSHPSIQLKK 122
 Db 143 LHLLTGDILKREVFVFCM-SFVQODDSNNKIPVYIGKOKNLVYSCVMKD--NTPTLQ-- 196
 QY 123 EKLMKLAQKESARPPIFIYRAQVGSMMLSEAHPGMFICTSNCNCNEPV 172
 Db 197 EDIDPKYKPKDMEKRVFVYKTEIKNRVFEFESALYPNWYISTSQAEQKPV 246
 RESULT 10
 S35969 interleukin-1 beta precursor - mouse
 N;Alternate names: hematopoietin-1; IL-1 beta
 C;Species: Mus musculus (house mouse)
 C;Date: 26-Jul-1996 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999
 C;Accession: I55969; A24719; S13029
 R;Gray, P.W.; Glaister, D.; Chen, E.; Goeddel, D.V.; Pennica, D.
 J. Immunol. 137, 3644-3648, 1986
 A;Title: Two interleukin 1 genes in the mouse: Cloning and expression of the cDNA for mu
 A;Reference number: I55969; MUID:87058957; PMID:3491144
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-269 <REB>
 A;Cross-references: GB:MI5131; NID:9198293; PIDN:AAA39276.1; PID:9309398

Relford, J.L.; Macchia, G.; Massone, A.; Carinci, V.; Palla, B.; Melli, M.; Nucleic Acids Res. 14, 9955-9963, 1986
 A;Title: The murine interleukin-1-beta Gene: structure and evolution.
 A;Accession: A24719; MUID:87117546; PMID:3492706
 A;Molecule type: mRNA
 A;Residues: 1-269 <TEL>
 A;Cross-references: GB:XA04964; NID:95266; PIDN:CAA28637.1; PID:952667
 R;Daumy, G.O.; Wilder, C.L.; Merenda, J.M.; McColl, A.S.; Geoghegan, K.F.; Otterness, I.
 FEBS Lett. 278, 98-102, 1991
 A;Title: Reduction of biological activity of murine recombinant interleukin-1beta by self-
 A;Reference number: S13029; MUID:91130610; PMID:1993481
 A;Accession: S13029
 A;Status: preliminary
 A;Molecule type: Protein
 A;Residues: 118-269 <DAU>
 C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavage
 form of interleukin-1beta, unlike interleukin-1-alpha, is inactive.
 C;Genetic: IL-1-beta
 C;Superfamily: interleukin-1
 C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
 F:118-269/Product: interleukin-1 beta #status experimental <IL1>
 Query Match 11 4%; Score 120 5; DB 1; Length 269;
 Best Local Similarity 27.8%; Pred. No. 0.0011_79; Indels 17; Gaps 9;
 Matches 50; Conservative 34; Mismatches 17;
 Qy 14 VADYKDDDKLAAANASALCRGPKVNLNPKKPSIHDQDHKLVL-DSGNLIAPV-DKNTI 71
 Db 103 LDLSWDDDD----NLLVCDVP-IRRQLH--YRDLDEQPKSLVLSDPYELKALHNGQNTI 153
 Qy 72 RPEIFFALASSLSSSAEKAQSPILLGVSKGEFLCLYCDKDKQSHPSLQLKREKUNKLAAQ 131
 Db 154 NQQVITFSMRFVQGGSNSDK-1PVAILGLKGKNUYLISCVWMDGT--PTLQL--ESDPKQYR 208
 Qy 132 KESARRPFFYRAQGWSWNMLESAAHPGWFICTSNCNCNBPVGVMTDKFENRKHTEFSFQPY 191
 Db 209 KKKWEEKRKFVNKEVVKSKVFEFSAEFPNWYISTSOAEHKPVFLGNNS-GQDIDPTEMSY 267
 ICB01B
 interleukin-1 beta precursor - bovine
 N;Alternative names: hematopoietin-1; IL-1 beta
 C;Species: Bos primigenius taurinus (cattle)
 C;Date: 31-Mar-1999 #sequence_revision 31-Mar-1999 #text_change 22-Jun-1999
 C;Accession: JL0010; S01380
 R;Maliszewski, C.R.; Baker, P.E.; Schoenborn, M.A.; Davis, B.S.; Cosman, D.; Gillis, S.;
 Mol. Immunol. 25, 429-437, 1988
 A;Title: Cloning, sequence and expression of bovine interleukin-1-alpha and interleukin-1
 A;Reference number: A94695; MUID:88318652; PMID:3261832
 A;Accession: JL0010
 A;Molecule type: mRNA
 A;Residues: 1-266 <WAL>
 A;Cross-references: GB:NM37211; NID:9163200; PIDN:AAA10584.1; PID:9163201
 R;Leong, S.R.; Flagg, G.M.; Lawman, M.; Gray, P.W.
 Nucleic Acids Res. 16, 9054, 1988
 A;Title: The nucleotide sequence for the cDNA of bovine interleukin-1-alpha and interleukin-1
 A;Reference number: S01380; MUID:89016591; PMID:3262866
 A;Accession: S01380
 A;Molecule type: mRNA
 A;Residues: 1-251, A', 253-266 <LEO>
 A;Cross-references: EMBL:XI1498; NID:9448; PIDN:CAA31018.1; PID:9449
 C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavage
 form of interleukin-1beta, unlike interleukin-1-alpha, is inactive.
 C;Superfamily: interleukin-1
 C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
 F:114-266/Product: interleukin-1 beta #status predicted <WAL>

Query Match 11 1%; Score 118; DB 1; Length 266;
 Best Local Similarity 25 4%; Pred. No. 0.0018; Mismatches 46; Conservative 33; Mismatches 46; Matches 46; Insertions 26; Gaps 8;

Qy	9	LVGAGAVADYKDDDDLA-----AANSA	LCRGPKVNLPKKFSINDQDHK	53
Db	.	LRNSAVAHVFHDIDRSLSFIFEEBEPVIFETSSBFLCDAP-VQSI--KCKLGDR	EQ	129
Qy	54	VLVLDSGNLTAVPD--KNYIRPEIFALASSLSSA	KECSPILIGVSKGEFCLYCDKDK	111
Db	130	SLVLASPCVULKALHLSQENRREVFCM-SFVQGERD	KPVALGIKDRNLYLSCVK-K	187
Qy	112	GOSHSLQLKKEKMLAAKESAFARSPF	YRAQGWSWNMLESAMHPGWICTSNCNEP	171
Db	188	GDT-PIQL--EEVDPKVYPRNNMKEFRVYKTEKNTVPEFSLVLPNWYISTSQI	ERP	244
Qy	172	V 172		
Db	245	V 245		

RESULT 12

ICHUHB

interleukin-1 beta precursor [validated] - human

N;Alternate names: hematopoietin-1; IL-1 beta

C;Species: Homo sapiens (man)

C;Date: 28-Feb-1986 #sequence revision 15-May-1998 #text_change 15-Sep-2000

C;Accession: A25542; A22019; A94023; A93361; I15852; I15200; I18132; B27616; A01848; S19

R;Clark, B.D.; Collins, K.L.; Gandy, M.S.; Webb, A.C.; Aucion, P.E.

Nucleic Acids Res. 14, 7897-7914, 1986

A;Title: Genomic sequence for human prointerleukin 1 beta: possible evolution from a rev

A;Reference number: A25542; MUID:8704052; PMID:3490654

A;Accession: A25542

A;Molecule type: DNA; mRNA

A;Residues: 1-5, 'K', 7-69 <CDA>

A;Cross-references: GB:X04500; NID:933788

A;Note: the mRNA sequence had codon AAG for 6-Lys, the DNA sequence had GAG for 6-Glu

R;Bensi, G.; Raugei, G.; Palla, E.; Carrinci, V.; Buonamassa, D.T.; Melli, M.

Gene 52, 95-101, 1987

A;Title: Human interleukin-1 beta gene

A;Reference number: A29019; MUID:87248099; PMID:2954882

A;Accession: A29019

A;Molecule type: DNA

A;Residues: 1-269 <EBN>

A;Cross-references: GB:MI15840; NID:9186281; PIDN:AAA74137_1; PID:9386816

R;March, P.E.; Webb, A.C.; Rosennasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Dinare

Proc. Natl. Acad. Sci. U.S.A. 81, 7907-7911, 1984

A;Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.

A;Reference number: A94023; MUID:85088517; PMID:6083565

A;Accession: A94023

A;Molecule type: mRNA

A;Residues: 1-5, 'K', 7-269 <AU>

A;Cross-references: GB:K02770; NID:9186268; PIDN:AAA36106_1; PID:9307043

R;March, C.J.; Mosley, B.; Larsen, A.; Cerretti, D.P.; Braedt, G.; Price, V.; Gillis, S.

Nature 315, 641-647, 1985

A;Title: Cloning, sequence and expression of two distinct human interleukin-1 complement

A;Reference number: A93361; MUID:85240547; PMID:2989698

A;Accession: A93361

A;Molecule type: mRNA

A;Residues: 1-269 <MAR>

A;Accession: 151852

A;Statusus: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-5, 'K', 7-19, 'H', 21-110, 'Q', 112-176, 'A', 178-213, 'P', 215-269 <WEB>

A;Cross-references: GB:MI54913; NID:gi86287; PIDN:AA59136_1; PID:gi86288

R;Webb, A.C.; Dinarollo, C.A.; Rosennasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Au

Adv. Gene Technol. 22, 339-40, 1985

A;Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.

A;Reference number: 151852

A;Title: cDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell line.
 A;Reference number: 152217; MUID:87156769; PMID:3493774
 A;Accession: 162200
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residue: 1-269 <NLS>
 A;Cross-references: GB:MI5330; NID:9186283; PIDN:AA59135.1; PID:9307045
 R;Kotenko, S.V.; Bulekov, M.T.; Veiko, V.P.; Epishin, S.M.; Lomakin, I.B.; Emel'yanov, S.A.; Vinetskii, Y.P.
 Dokl. Akad. Nauk SSSR 309, 1005-1008, 1989
 A;Title: [Cloning of the cDNA coding for human prointerleukin-1 alpha and prointerleukin-1 beta]
 A;Reference number: 138131; MUID:90349285; PMID:2635664
 A;Accession: 13132
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-269 <NLS>
 A;Cross-references: EMBL:Y56087; NID:935662; PIDN:CAA39567.1; PID:935663
 R;Zsebo, K.M.; Wypych, J.; Yuschenko, V.N.; Lu, H.; Hunt, P.; Dukes, P.P.; Langley, K.
 Blood 71, 962-968, 1988
 A;Title: Effects of hematopoietin-1 and interleukin 1 activities on early hematopoietic progenit. Natl. Acad. Sci. U.S.A. 90, 7245-7249, 1993
 A;Reference number: A90732; MUID:88184226; PMID:3281727
 A;Accession: B7616
 A;Molecule type: protein
 A;Residues: 117-123, 'X', 125-126, 'X', 128 <ZSE>
 R;Stevenson, F.T.; Bursten, S.L.; Fenton, C.; Locksley, R.M.; Lovett, D.H.
 Proc. Natl. Acad. Sci. U.S.A. 86, 7457-7459, 1989
 A;Title: The 31-kDa precursor of interleukin 1alpha is myristoylated on specific lysines
 A;Reference number: A48293; MUID:9348250; PMID:8346241
 A;Contents: annotation; myristylation of lysine
 R;Nanduri, V.B.; Hulmes, J.D.; Pan, Y.C.E.; Kilian, P.L.; Stern, A.S.
 Biochim. Biophys. Acta 1118, 25-35, 1991
 A;Title: The role of arginine residues in interleukin 1 receptor binding.
 A;Reference number: 519608; MUID:92110334; PMID:1837236
 A;Contents: annotation; type 1 IL-1 receptor interaction site
 A;Note: modification of Arg-120 by phenylglyoxal blocks receptor binding
 R;Clore, G.M.; Gronenborn, A.M.
 submitted to the Brookhaven Protein Data Bank, January 1991
 A;Reference number: A50049; MUID:6161B
 A;Contents: annotation; conformation by (13)C- and (1)H-NMR, residues 117-269
 R;Clore, G.M.; Wingfield, P.T.; Gronenborn, A.M.
 Biochemistry 30, 2315-2323, 1991
 A;Title: High-resolution three-dimensional structure of interleukin 1beta in solution by
 A;Reference number: A44675; MUID:91159409; PMID:2001363
 A;Contents: annotation; (1)H-NMR structural determination
 R;Hazuda, D.J.; Strickler, J.; Simon, P.; Young, P.R.
 J. Biol. Chem. 266, 7081-7086, 1991
 A;Title: Structure-function mapping of interleukin 1 precursors. Cleavage leads to a core
 A;Reference number: A93774; MUID:91201363; PMID:2016316
 A;Contents: annotation
 R;Finzel, B.C.; Watengaugh, K.D.; Binspahr, H.M.
 submitted to the Brookhaven Protein Data Bank, December 1989
 A;Reference number: A50016; PDB:111B
 A;Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 119-269
 R;Finzel, B.C.; Clancy, L.L.; Holland, D.R.; Muchmore, S.W.; Watengaugh, K.D.; Binspahr, J. Mol. Biol. 209, 779-791, 1989
 A;Title: Crystal structure of recombinant human interleukin-1beta at 2.0 angstrom resolution
 A;Reference number: A54666; MUID:9004532; PMID:2585509
 A;Contents: annotation; X-ray crystallography, 2.0 angstroms
 C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavage of interleukin-1beta, unlike interleukin-1-alpha, is inactive.
 C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1alpha.
 C;Genetics: GDB:111B
 A;Cross-references: GDB:120094; OMIM:147720
 A;Map position: 2q13-q21
 A;Introns: 16/2; 33/3; 101/1; 156/1; 199/3
 C;Superfamily: interleukin-1
 C;Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophag
 F:117-269/Product: interleukin-1 beta #status experimental <in>
 F:76/Binding site: myristate (Lys) (covalent) (partial) #status experimental
 F:123/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match

9.3%; Score 98; DB 1; Length 269;

Best Local Similarity 28.0%; Pred. No. 0.14;
 Matches 42; Conservative 27; Mismatches 65; Indels 16; Gaps 8;
 Qy B25528
 Db 110 NEAVYVDAPIVSVN--CTTURSDQQSILV-SGPVFLKALHQLQGQDMEQQVFSMVQ 165
 Qy 85 SASAEKSPILGVNSKGECFLYC--DKDKGOSHPSIQLKKKLMKLAQESARRPFY 142
 Db 166 EESNDK-1PVAGLKGKLVISCVLKKD---PRLQL--ESVDPKNNPKKKMKEKPVEN 218
 Qy 143 RAQVGSHMMLMELSAHPOGWFICTSNCNCNPV 172
 Db 219 KIEINNKLEFESAQFPNWWYISTSOAENMPV 248

RESULT 13
 B25528
 C;Species: Mus musculus (house mouse)
 C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 22-Jun-1999
 C;Accession: B25528
 R;Stevenson, B.J.; Hagenbuchle, O.; Wellauer, P.K.
 Nucleic Acid Res. 14, 8307-8330, 1986
 A;Residues: 1-246 <STE>
 A;Cross-references: GB:X04574; NID:954918; PIDN:CAA28243.1; PID:954919.
 C;Superfamily: trypsin; trypsin homology
 C;Keywords: calcium binding; hydrolase; protein digestion; serine proteinase
 C;1-23;Domain: signal sequence #status predicted <SIG>
 F:24-246/Product: trypsin #status predicted <MAT>
 F:24-239/Domain: trypsin homology <TRY>
 F:30-160, 48-64, 132-233, 138-206, 171-185/disulfide bonds: #status predicted
 F:75, 77, 80-85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
 Query Match 1 MSALLILALVGAVADYKDDDKLAAANSALCRGPVKWNLNPKFS-----IH 48
 Db 1 MSALLILALVGAVADYKDDDKLAAANSALCRGPVKWNLNPKFS-----IH 48
 Qy 49 DQ-----DHKVLNL-----DSCNLAVPDKN 69
 Db 55 DQWVSAHCVKYRIQVRLGEHNINVLEGNBQFVDSAKITRHPNVN 100

RESULT 14
 A30584
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 25-May-1994 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999
 C;Accession: A27714; A30584; JID:0082; A31616
 R;Mori, S.; Goto, F.; Goto, K.; Ohkawara, S.; Maeda, S.; Shimada, K.; Yoshinaga, M.
 Biochem. Biophys. Res. Commun. 150, 1231-1243, 1988
 A;Title: Cloning and sequence analysis of a cDNA for lymphocyte proliferation potentiatir
 A;Reference number: A27714; MUID:88134238; PMID:2449207
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-268 <NOR>
 R;Cannon, J.G.; Clark, B.D.; Wingfield, P.; Schmeisser, U.; Losberger, C.; Dinarello, C.
 J. Immunol. 142, 2293-2306, 1989
 A;Title: Rabbit IL-1. Cloning, expression, biologic properties, and transcription during
 A;Reference number: A30584; MUID:89176242; PMID:2784458
 A;Accession: A30584
 A;Molecule type: mRNA

A;Residues: 1-268 <CAN>
 A;Cross-references: GB:M26295; NID:9516632; PID:9516633
 R;Youn, P.R.; Sylvester, D.
 Protein Eng. 2, 545-551, 1989
 A;Title: Cloning of rabbit interleukin-1 beta: differential evolution of IL-1 alpha and
 A;Reference number: A91230; MUID:9915118; PMID:2787507
 A;Accession: JU0082
 A;Molecule type: mRNA
 A;Residues: 1-268 <YOU>
 C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavage
 form of interleukin-beta, unlike interleukin-1-alpha, is inactive.
 C;Superfamily: interleukin-1
 C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen.
 F;117-268/Product: interleukin-1 beta #status predicted <ILB>

Query Match 8.7%; Score 92.5; DB 1; length 268;
 Best Local Similarity 24.7%; Pred No. 0.44; DB 1;
 Matches 44; Conservative 26; Mismatches 81; Indels 27; Gaps 7;
 Qy 16 DYKDDDKLAAANSALCRGPKVKLNPKKSIHDQHKVLYLDSSNLIAVPDFN--YIRP 73
 Db 110 DYSLECD--AVRSLHCR-----LQDAQKSLVLSGTYELKALHLWAENLQ 153
 Qy 74 BIFFALASSLSSASAEGSPFLPLGVSKGFCFLYC--DKDKGQSHSLQLKKLMLKLAQ 131
 Db 154 QVVFMSFVQOESNDK-IPVALGLRGKNTYLSCWIKDDK---PTLQL--ESVDPNRP 206
 Qy 132 KESARRPPIFYRAQGWSWNLLESAAHPGWICCTSCNCNEVGVGVTDKFENRKHIFSFQ 189
 Db 207 KKKMERRFVFNKIEIKDKLEFESAOPNWYISTSQTEYMPVFLGNNSG3QDLDIFSM 264

RESULT 15

S34031 KTR3 protein - yeast (Saccharomyces cerevisiae)
 N;Alternate names: protein YBR1447; protein YBR205W
 C;Species: Saccharomyces cerevisiae
 C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 07-May-1999
 C;Accession: S34031; S46077; S34928
 R;Jacquet, M.
 R;Submitted to the EMBL Data Library, January 1993
 A;Reference number: S34022
 A;Accession: S34031
 A;Molecule type: DNA
 A;Residues: 1-404 <JAC>
 A;Cross-references: EMBL:Z21487; NID:9311665; PID:9311682
 R;Buserreau, P.; Demolins, M.; Jacquet, M.; Mallet, L.
 R;Submitted to the Protein Sequence Database, August 1994
 A;Reference number: S46054
 A;Accession: S46077
 A;Molecule type: DNA
 A;Residues: 1-404 <BUS>
 A;Cross-references: EMBL:Z36074; NID:9536582; PID:9536583; MIPS:YBR205W
 R;Buserreau, F.; Mallet, L.; Gaillon, L.; Jacquet, M.
 Yeast 9, 797-806, 1993
 A;Title: Yeast Sequencing Reports, A 12.8 kb segment, on the right arm of chromosome II
 A;Reference number: S34925; MUID:93377417; PMID:8368014
 A;Accession: S34928
 A;Molecule type: DNA
 A;Residues: 91-352 <BU2>
 A;Cross-references: EMBL:Z21487
 C;Genetics:
 A;Gene: SGD:KIR3
 A;Cross-references: SGD:S0000409; MIPS:YBR205W
 A;Map position: 2R
 C;Keywords: transmembrane protein
 F;22-45/Domain: transmembrane #status predicted <TM>

Query 46 SINDODHKVLYLDSGNLIAVPDFNIRE-----IFFALASSSSASAEGSPIL 95
 Db 2 SVH---HKKCLMPKSALLIRKYQCGIRSSPFIGLIVLSSLFFMSGSRSPVPIAGTSVS 58
 Qy 96 LGVSKGECFLYCDKDGKOSHPSLQGKKEKLMKLAQESARRPPFIFYRAQVGSMNMLESA 155
 Db 59 RVASKDYLMPFTDKSOGVLRHPVDDGKKEKGVMVTLARS-----DLWNLVKSI 106
 Qy 156 AHPGMFICFSCNCNCBPGVTDKFNKRHIEFSP---QP 190
 Db 107 RH-----TDFRNNRHYDWFVFLNDOP 128
 Search completed: September 9, 2004, 13:28:28
 Job time : 42 secs

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